

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: April 11, 2001, 14:01:44 ; Search time 20.34 Seconds  
(without alignments)  
132.536 Million cell updates/sec

Title: US-09-164-223-2

Perfect score: 123

Sequence: 1 PSQASSGQARMPNAPYLPSGLE 23

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: SPREMBL.15:\*  
2: sp.archaea:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.rodent:\*  
12: sp.virus:\*  
13: sp.vertebrate:\*  
14: sp.unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	123	100.0	446	4 Q15881	Q15881 homo sapien
2	103	83.7	407	13 P79958	P79958 xenopus lae
3	102	82.9	390	13 Q42223	Q42223 trachemys s
4	99	80.5	392	13 Q91030	Q91030 gallus gall
5	99	80.5	414	13 Q918A1	Q918A1 gallus gall
6	99	80.5	417	13 Q918A0	Q918A0 gallus gall
7	95	77.2	409	13 Q91657	Q91657 xenopus lae
8	85	69.1	426	13 Q9W611	Q9W611 cynops pyr
9	82	66.7	392	13 Q91BR0	Q91BR0 anguilla ja
10	65	52.8	392	13 Q93433	Q93433 fugu rubrip
11	63	51.2	419	13 Q9P077	Q9P077 brachydanio
12	48	39.0	188	4 Q16591	Q16591 homo sapien
13	48	39.0	188	4 Q14901	Q14901 paramesclum
14	48	39.0	778	12 Q84509	Q84509 paramesclum
15	47.5	38.6	65	6 Q46611	Q46611 bubalus bub
16	47	38.2	250	4 Q95417	Q95417 homo sapien
17	47	38.2	115	5 Q16031	Q16031 harmothoe i
18	47	38.2	405	10 Q41516	Q41516 triticum ae
19	47	38.2	405	10 Q95XY0	Q95XY0 triticum ae

20	47	38.2	815	10 Q41553	Q41553 triticum ae
21	47	38.2	830	10 Q03872	Q03872 triticum ae
22	47	38.2	3381	2 Q9KX33	Q9KX33 streptococ
23	46	37.4	374	5 Q26665	Q26665 sternaspis
24	46	37.4	606	8 Q9TA19	Q9TA19 loxodonta a
25	46	37.4	766	10 Q9SDM3	Q9SDM3 triticum ae
26	46	37.4	955	11 Q88287	Q88287 mus musculu
27	45.5	37.0	704	5 Q45750	Q45750 caenorhabd
28	45	36.6	320	2 Q56299	Q56299 thiodacillu
29	45	36.6	381	10 Q41556	Q41556 triticum ae
30	45	36.6	385	2 Q54913	Q54913 streptococ
31	45	36.6	388	14 Q35997	Q35997 planoprotos
32	45	36.6	401	14 Q35996	Q35996 planoprotos
33	45	36.6	488	5 Q9TYR3	Q9TYR3 caenorhabd
34	45	36.6	572	11 Q61090	Q61090 mus musculu
35	45	36.6	2075	5 Q9VXY2	Q9VXY2 deet pseudo
36	44	35.8	225	12 P87542	P87542 beet helicobact
37	44	35.8	292	2 Q25957	Q25957 helicobacte
38	44	35.8	292	2 Q92UK7	Q92UK7 helicobacte
39	44	35.8	343	5 Q18636	Q18636 musca domes
40	44	35.8	393	5 Q18880	Q18880 caenorhabd
41	44	35.8	395	5 Q26913	Q26913 trypanosoma
42	44	35.8	449	5 Q00819	Q00819 trypanosoma
43	44	35.8	455	5 Q31345	Q31345 bacillus ce
44	44	35.8	459	5 Q9U5V4	Q9U5V4 dreissena p
45	44	35.8	472	10 Q95NS0	Q95NS0 arabidopsis

## ALIGNMENTS

RESULT 1  
ID Q15881 PRELIMINARY: PRT; 446 AA.  
AC Q15881:  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
DE WILMS TUMOR PROTEIN.  
GN WT1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92241883; PubMed=1572653;  
RA Gessler M., Konig A., Bruns G.A.;  
RT "The genomic organization and expression of the WT1 gene.";  
RT Genomics 12:807-813(1992).  
DR EMBL: X61631; CAA43819.1; JOINED.  
DR EMBL: X61632; CAA43819.1; JOINED.  
DR EMBL: X61633; CAA43819.1; JOINED.  
DR EMBL: X61634; CAA43819.1; JOINED.  
DR EMBL: X61635; CAA43819.1; JOINED.  
DR EMBL: X61636; CAA43819.1; JOINED.  
DR EMBL: X61637; CAA43819.1; JOINED.  
DR EMBL: X61638; CAA43819.1; JOINED.  
DR HSSP: P08046; 1AAV.  
DR INTERPRO: IPR000822; -  
DR INTERPRO: IPR000976; -  
DR PFM: PFM0096; z1-C2H2; 4.  
DR PFM: PFM0165; WT1; 1.  
DR PRINTS: PRO0048; ZINCINGER.  
DR PRINTS: PRO0049; WILMSTUMOUR.  
DR PROSITE: PS00028; ZINC\_FINGER\_C2H2; 4.  
DR ZINC\_FINGER; Metal-binding; DNA-binding.  
KW SEQUENCE 446 AA; 48842 MW; 8CEVFC047FA1CF11 CRC64;

Query Match 100.0%; Score 123; DB 4; Length 446;  
Best Local Similarity 100.0%; Pred. No. 2e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PSQASSGQARMPNAPYLPSCLE 23  
 DB 117 PSQASSGQARMPNAPYLPSCLE 139

RESULT 2  
 ID P79958 PRELIMINARY; PRT; 407 AA.  
 AC P79958;

DT 01-MAY-1997 (TREMBlrel. 03, Created)  
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
 DE WT1 PROTEIN.

GN WT1.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodidae; Xenopus.  
 OX NCBI\_TaxID=8355;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=TESTIS;  
 RX MEDLINE=97074667; PubMed=9917094;  
 RA Senda K., Saito-Ueno R., Takayama G., Kondo M.;  
 RT "CDNA cloning and its pronephros-specific expression of the Wilms' tumor suppressor gene, WT1, from Xenopus laevis.";

RL Gene 175:167-172(1996).  
 DR EMBL: D82051; BAA11522.1; -;  
 DR HSSP: P08046; 1AAY.  
 DR INTERPRO: IPR000822; -;  
 DR TISSUE=WHOLE EMBRYO;  
 DR INTERPRO: IPR000976; -;  
 DR PFAM: PF00096; zf-C2H2; 4.  
 DR PFAM: PF02165; WT1; 3.

DR PRINTS: PR00048; ZINC\_FINGER.  
 DR PROSITE: PS00028; ZINC\_FINGER\_C2H2; 4.  
 DR Zinc-finger; Metal-binding; DNA-binding.  
 KW SEQUENCE 407 AA; 45983 MW; E2554C658005870C CRC64;

Query Match  
 Best Local Similarity 83.7%; Score 103; DB 13; Length 407;  
 Matches 18; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 PSQASSGQARMPNAPYLPSCLE 23  
 DB 98 PSQATTGQARMPNAPYLPSCLD 120

RESULT 3  
 ID 042223 PRELIMINARY; PRT; 390 AA.  
 AC 042223;

DT 01-JAN-1998 (TREMBlrel. 05, Created)  
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
 DE WT1MS TUMOR 1 PROTEIN.

GN WT1.  
 OS Trachemys scripta (Red-eared slider turtle).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Testudines; Cryptodira; Testudinoidae; Emydidae; Trachemys.  
 OX NCBI\_TaxID=34903;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=WHOLE EMBRYO;  
 RX MEDLINE=97074667; PubMed=9917094;  
 RA Senda K., Saito-Ueno R., Takayama G., Kondo M.;  
 RT "CDNA cloning and its pronephros-specific expression of the Wilms' tumor suppressor gene, WT1, from Xenopus laevis.";

RL Gene 175:167-172(1996).  
 DR EMBL: D82051; BAA11522.1; -;  
 DR HSSP: P08046; 1AAY.  
 DR INTERPRO: IPR000822; -;  
 DR TISSUE=WHOLE EMBRYO;  
 DR INTERPRO: IPR000976; -;  
 DR PFAM: PF00096; zf-C2H2; 4.  
 DR PFAM: PF02165; WT1; 2.  
 DR PRINTS: PR00048; ZINC\_FINGER.

DR PROSITE: PS00028; ZINC\_FINGER\_C2H2; 3.  
 KW Zinc-finger; Metal-binding; DNA-binding.  
 SQ SEQUENCE 390 AA; 43620 MW; 1C9987435B927C2 CRC64;

Query Match  
 Best Local Similarity 82.9%; Score 102; DB 13; Length 390;  
 Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 PSQASSGQARMPNAPYLPSCLE 23  
 DB 100 PTOAPSSQARMPNAPYLPSCL 122

RESULT 4  
 ID 091030 PRELIMINARY; PRT; 392 AA.  
 AC 091030;

DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
 DE CHICK WILM'S TUMOUR PROTEIN (FRAGMENT).

GN WT1.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=WHOLE EMBRYO;  
 RX MEDLINE=96068905; PubMed=7478606;  
 RA Kent J., Coriat A.M., Sharpe P.T., Hastie N., Van Heyningen V.;  
 RT "The evolution of WT1 sequence and expression pattern in the vertebrates.";

RL Oncogene 11:1781-1792(1995).  
 DR EMBL: X85731; CAA59736.1; -;  
 DR HSSP: P08046; 1AAY.  
 DR INTERPRO: IPR000822; -;  
 DR TISSUE=WHOLE EMBRYO;  
 DR INTERPRO: IPR000976; -;  
 DR PFAM: PF00096; zf-C2H2; 3.  
 DR PFAM: PF02165; WT1; 2.

DR PRINTS: PR00049; WILMS\_TUMOUR.  
 DR PROSITE: PS00028; ZINC\_FINGER\_C2H2; 3.  
 DR Zinc-finger; Metal-binding; DNA-binding.  
 KW NON\_TER 392  
 FT NON\_TER 392  
 SQ SEQUENCE 392 AA; 43869 MW; 761F01D350E4EDBF CRC64;

Query Match  
 Best Local Similarity 80.5%; Score 99; DB 13; Length 392;  
 Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 PSQASSGQARMPNAPYLPSCLE 23  
 DB 100 PSQPPSQARMPNAPYLPSCL 122

RESULT 5  
 ID 0918A1 PRELIMINARY; PRT; 414 AA.  
 AC 0918A1;

DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
 DE WT1(-KTS) PROTEIN.

GN WT1(-KTS).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]

RP SEQUENCE FROM N.A.  
RC TISSUE-Ovary;  
RA Kudo T.;  
RT "Chicken counterpart of Wilms' tumor suppressor gene 1.";  
RL Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AB033633; BAA94793.1; -  
SO SEQUENCE 414 AA; 46641 MW; 17EB22F8B428A2EF CRC64;

Query Match 80.5%; Score 99; DB 13; Length 414;  
Best Local Similarity 78.3%; Pred. No. 1.1e-07;  
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 PSQASSGQARMPNAPYLPSCLE 23  
DB 100 PSQPPSGQARMPORPYLPNCLE 122

RESULT 6  
OY18A0 PRELIMINARY; PRT; 417 AA.  
AC O918A0:  
DT 01-OCT-2000 (TREMblrel. 15, Created)  
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)  
DE WT1(+KTS) PROTEIN.  
GN WT1(+KTS).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-Ovary;  
RA Kudo T.;  
RT "Chicken counterpart of Wilms' tumor suppressor gene 1.";  
RL Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AB033634; BAA94794.1; -  
SO SEQUENCE 417 AA; 46957 MW; 47BBF7F6448E76C CRC64;

Query Match 80.5%; Score 99; DB 13; Length 417;  
Best Local Similarity 78.3%; Pred. No. 1.1e-07;  
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 PSQASSGQARMPNAPYLPSCLE 23  
DB 100 PSQPPSGQARMPORPYLPNCLE 122

RESULT 7  
OY1657 PRELIMINARY; PRT; 409 AA.  
AC O91657:  
DT 01-NOV-1996 (TREMblrel. 01, Created)  
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)  
DE WILMS' TUMOR SUPPRESSOR (WT1).  
GN WT1.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;  
OC Xenopodidae; Xenopus.  
OX NCBI\_TaxID=8335;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Carroll T.J., Vize P.D.;  
RL Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.  
RN [2]  
RP SEQUENCE OF 289-370 FROM N.A.  
RC TISSUE-MESONEPHROS;  
RX MEDLINE=96068905; PubMed=7478606;

RA Kent J., Coriat A.M., Sharpe P.T., Hastie N., Van Heyningen V.;  
RT "The evolution of WT1 sequence and expression pattern in the  
vertebrates."  
RL Oncogene 11:1781-1792(1995).  
DR EMBL: U42011; AAB53152.1; -  
DR EMBL: X85733; CAA59738.1; -  
DR HSSP: P08046; IAAV.  
DR INTERPRO: IPR000822; -  
DR INTERPRO: IPR000976; -  
DR PFAM: PF00096; ZF-C2H2; 4.  
DR PFAM: PF02165; WT1; 3.  
DR PRINTS: PR00048; ZINC\_FINGER\_C2H2; 4.  
DR PROSITE: PS00028; ZINC\_FINGER\_C2H2; 4.  
KW Zinc-finger: Metal-binding; DNA-binding.  
SO SEQUENCE 409 AA; 46186 MW; 2217FC04612CDE10 CRC64;

Query Match 77.2%; Score 95; DB 13; Length 409;  
Best Local Similarity 73.9%; Pred. No. 4.5e-07;  
Matches 17; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 PSQASSGQARMPNAPYLPSCLE 23  
DB 97 PSQATGQARMSNAPYLSNCLD 119

RESULT 8  
OY9611 PRELIMINARY; PRT; 426 AA.  
AC OY9611:  
DT 01-NOV-1999 (TREMblrel. 12, Created)  
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)  
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)  
DE WT1.  
OS Cynops pyrrhogaster (Japanese common newt).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Caudata; Salamandridae; Salamandridae; Cynops.  
OX NCBI\_TaxID=8330;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-TESTIS;  
RA Nakayama Y., Yamamoto T., Matsuda Y., Abe S.I.;  
RT "Cloning of cDNA for newt WT1 and the differential expression during  
spermatogenesis of the Japanese newt, Cynops pyrrhogaster."  
RL Submitted (MAY-1998) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AB013888; BAA76399.1; -  
DR HSSP: P08046; IAAV.  
DR INTERPRO: IPR000822; -  
DR INTERPRO: IPR000976; -  
DR PFAM: PF00096; ZF-C2H2; 4.  
DR PFAM: PF00096; ZF-C2H2; 4.  
DR PRINTS: PR00049; WILMSTUMOR.  
DR PROSITE: PS00028; ZINC\_FINGER\_C2H2; 4.  
KW Zinc-finger: Metal-binding; DNA-binding.  
SO SEQUENCE 426 AA; 47590 MW; 46A0B158A9F79C6C CRC64;

Query Match 69.1%; Score 85; DB 13; Length 426;  
Best Local Similarity 65.2%; Pred. No. 1.7e-07;  
Matches 15; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 PSQASSGQARMPNAPYLPSCLE 23  
DB 107 PSQPPAQVARMPSNGPYLPNCLE 129

RESULT 9  
OY1BF0 PRELIMINARY; PRT; 392 AA.  
AC O91BF0:  
DT 01-OCT-2000 (TREMblrel. 15, Created)  
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)  
DE WILMS' TUMOR PROTEIN.

GN EMT1.  
 OS Anguilla japonica (Japanese eel).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;  
 OC Anguilla.  
 NCBI\_TaxID=7937;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=KIDNEY.  
 RA Nakatsu Y., Minami K., Yoshikawa A., Zhu J.-J., Oda H., Masahito P.,  
 RA Okamoto N., Nakamura Y., Ishikawa T.;  
 RT "Bel Wt1 sequence and expression in spontaneous nephroblastomas in  
 RT Japanese eel."  
 RL Gene 245:245-251(2000).  
 DR EMBL: AB030741; BAA0558.1;  
 SO SEQUENCE 392 AA; 43892 MW; DAELA84828F43DF6 CRC64;

Query Match 66.7%; Score 82; DB 13; Length 392;  
 Best Local Similarity 60.9%; Pred. No. 4.8e-05;  
 Matches 14; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
 Oy 1 PSQSSGQARMFPNAPYLPSCLE 23  
 Db 103 PSQPPGNQARMFANGPYLPNCVD 125

RESULT 10  
 093433 PRELIMINARY; PRT; 416 AA.  
 AC 093433;  
 DT 01-NOV-1998 (TREMblrel. 08, Created)  
 DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)  
 DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)  
 DE WILMS TUMOUR GENE.  
 GN WT1.  
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostomi;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
 OC Tetraodontidae; Takifugu.  
 NCBI\_TaxID=31033;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RA Miles C., Elgar G., Coles E., Kleinjan D.J., Vanheyningen V.,  
 RA Hastie N.;  
 RT "Complete sequencing of the Fugu WAGR region from WT1 to PAX6  
 RT -dramatic compaction and conservation of synteny with human chromosome  
 RT 11p13."  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL021531; CA16491.1;  
 DR HSSP: P08046; IAAV.  
 DR INTERPRO: IPR000822; -;  
 DR INTERPRO: IPR000976; -;  
 DR PFAM: PF00096; zF-C2H2; 4.  
 DR PFAM: PF02165; WT1; 2.  
 DR PRINTS: PR00048; ZINC\_FINGER.  
 DR PROSITE: PS00028; ZINC\_FINGER\_C2H2; 4.  
 KW Zinc-finger; Metal-binding; DNA-binding.  
 SO SEQUENCE 416 AA; 45806 MW; 9C362E1684E67668 CRC64;

Query Match 52.8%; Score 65; DB 13; Length 416;  
 Best Local Similarity 61.1%; Pred. No. 0.024;  
 Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 6 SGQARMFPNAPYLPSCLE 23  
 Db 104 AGQPRMFPNGTCLPSCMD 121

RESULT 11  
 09PUT7

ID 09PUT7 PRELIMINARY; PRT; 419 AA.  
 AC 09PUT7;  
 DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)  
 DE WILMS' TUMOR SUPPRESSOR.  
 OS Brachydanio rerio (zebrafish) (zebra danio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
 OC Cypriniformes; Cyprinidae; Rasbora; Danio.  
 NCBI\_TaxID=7955;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RA Smith S.I., Down M., Power M., Boyd A.W.;  
 RT "Isolation and characterization of a cDNA encoding zebrafish (Danio  
 RT rerio) WT-1."  
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF144550; AAF00123.1;  
 DR HSSP: P08046; IAAV.  
 DR INTERPRO: IPR000822; -;  
 DR INTERPRO: IPR000976; -;  
 DR PFAM: PF00096; zF-C2H2; 4.  
 DR PFAM: PF02165; WT1; 3.  
 DR PRINTS: PR00049; WILMTUMOUR.  
 DR PROSITE: PS00028; ZINC\_FINGER\_C2H2; 4.  
 SO SEQUENCE 419 AA; 46925 MW; 606ADFEDA619ECD CRC64;

Query Match 51.2%; Score 63; DB 13; Length 419;  
 Best Local Similarity 50.0%; Pred. No. 0.049;  
 Matches 11; Conservative 4; Mismatches 7; Indels 0; Gaps 0;  
 Oy 2 SQSSGQARMFPNAPYLPSCLE 23  
 Db 103 SQPPSQPRMFSNPYLSNCMD 124

RESULT 12  
 016591 PRELIMINARY; PRT; 188 AA.  
 AC 016591;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)  
 DE C-MYC ONCOGENE, EXON 1.  
 GN MYC.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=87048763; PubMed=3778453;  
 RA Eladad M.E., Syed S.H., Guilhot S., d'Auriol L., Galibert F.;  
 RT "On the high conservation of the human c-myc first exon."  
 RL Biochem. Biophys. Res. Commun. 140:313-319(1986).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=84182501; PubMed=6714223;  
 RA Gazin C., De Dinechin S., Hampe A., Maesson J.M., Martin P.,  
 RA Stehelin D., Galibert F.;  
 RT "Nucleotide sequence of the human c-myc locus: provocative open  
 RT reading frame within the first exon."  
 RL EMBO J. 3:383-387(1984).  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=LEUKEMIA;  
 RX MEDLINE=88203638; PubMed=2834731;  
 RA Finver S.N., Nishikura K., Finger L.R., Haluska F.G., Finan J.,  
 RA Nowell P.C., Croce C.M.;  
 RT "Sequence analysis of the MYC oncogene involved in the  
 RT t(8;14)(q24;q11) chromosome translocation in a human leukemia T-cell  
 RT line indicates that putative regulatory regions are not altered."

RL Proc. Natl. Acad. Sci. U.S.A. 85:3052-3056(1988).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PROMYELOCYTIC LEUKEMIA;  
 RX MEDLINE=87089682; PubMed=3540591;  
 RA Bentley D.L., Groudine M.;  
 RT "Novel promoter upstream of the human c-myc gene and regulation of c-  
 myc expression in B-cell lymphomas."  
 RL Mol. Cell. Biol. 6:3481-3489(1986).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=84170251; PubMed=6324175;  
 RA Saito H., Hayday A.C., Wiman K.G., Tonegawa S.;  
 RT "Activation of the c-myc gene by translocation: a model for  
 translational control."  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:7476-7480(1983).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87053865; PubMed=2430795;  
 RA Gazin C., Rigoleit M., Briland J.P., Van Regenmortel M.H.V.,  
 RA Galibert F.;  
 RT "Immunochemical detection of proteins related to the human c-myc exon  
 1."  
 RL EMBO J. 5:2241-2250(1986).  
 DR EMBL: M14206; AAA88090.1; -;  
 DR EMBL: J00120; AAA20041.1; -;  
 DR EMBL: J03253; AAA59887.1; -;  
 DR EMBL: M13930; AAA88094.1; -;  
 DR EMBL: X00364; CAA25105.1; -;  
 SQ SEQUENCE 188 AA; 20955 MW; 677ADDDAC541477B CRC64;

Query Match 39.0%; Score 48; DB 4; Length 188;  
 Best Local Similarity 72.7%; Pred. No. 5;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 13 PNPAPLPSCLE 23  
 Db 22 PGRWPLPSCLE 32

RESULT 13  
 ID 014901 PRELIMINARY; PRT; 188 AA.  
 AC 014901;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
 DE MYC PROTEIN.  
 GN MYC.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LEUKEMIA;  
 RX MEDLINE=88203638; PubMed=2834731;  
 RA Flinter S.N., Nishikura K., Finger L.R., Haluska F.G., Finan J.,  
 RA Nowell P.C., Croce C.M.;  
 RT "Sequence analysis of the MYC oncogene involved in the  
 t(8;14)(q24;q11) chromosome translocation in a human leukemia T-cell  
 line indicates that putative regulatory regions are not altered."  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:3052-3056(1988).  
 DR EMBL: M20605; AAA59886.1; -;  
 SQ SEQUENCE 188 AA; 21050 MW; 9764637FDF79B00 CRC64;

Query Match 39.0%; Score 48; DB 4; Length 188;  
 Best Local Similarity 72.7%; Pred. No. 5;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 13 PNPAPLPSCLE 23

Db 22 PGRWPLPSCLE 32  
 RESULT 14  
 ID 084509 PRELIMINARY; PRT; 778 AA.  
 AC 084509;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
 DE PRO-RICH.  
 GN A189R.  
 OS Paramyxium bursaria chlorella virus 1 (PBCV-1).  
 OC Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phycodnavirus.  
 OC NCBI\_TaxID=10506;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95133167; PubMed=7831789;  
 RA Lu Z., Li Y., Zhang Y., Kutish G.F., Rock D.L., Van Etten J.L.;  
 RT "Analysis of 45 kb of DNA located at the left end of the chlorella  
 virus PBCV-1 genome."  
 RL Virology 206:339-352(1995).  
 DR EMBL: U42580; AAC96557.1; -;  
 SQ SEQUENCE 778 AA; 84593 MW; 166C087E14632662 CRC64;

Query Match 39.0%; Score 48; DB 12; Length 778;  
 Best Local Similarity 47.1%; Pred. No. 20;  
 Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 PSQASSGQARMFPNAPY 17  
 Db 170 PSQASAGLFFKNRPF 186

RESULT 15  
 ID 046611 PRELIMINARY; PRT; 65 AA.  
 AC 046611;  
 DT 01-JUN-1998 (TREMBlrel. 06, Created)  
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN TYPE 5 (FRAGMENT).  
 OS Bubalus bubalus (water buffalo).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bubalus.  
 OC NCBI\_TaxID=89462;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RIVER TYPE (MURRHA); TISSUE=OVARY;  
 RA Beg M.A., Appa Rao K.B.C., Torey S.M.;  
 RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF045566; AAC02555.1; -;  
 DR INTERPRO: IPR000716; -;  
 DR PFAM: PF00086; thyroglobulin\_1; 1.  
 DR PROSITE: PS00484; THYROGLOBULIN\_1; 1.  
 FT NON\_TER 1 65  
 FT NON\_TER 1 65  
 SQ SEQUENCE 65 AA; 7547 MW; DD2A79A681BF4530 CRC64;

Query Match 38.6%; Score 47.5; DB 6; Length 65;  
 Best Local Similarity 55.0%; Pred. No. 2.1;  
 Matches 11; Conservative 2; Mismatches 4; Indels 3; Gaps 1;

QY 2 SOASSGQARMFPNAPYLPSC 21  
 Db 1 AQAS---PRMVPRAYVLPNC 17

Search completed: April 11, 2001, 14:03:42  
Job time: 118 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: April 11, 2001, 14:01:59 ; Search time 8.66 Seconds  
(without alignments)  
85.770 Million cell updates/sec

Title: us-09-164-223-2

Sequence: 1 PSQASSSQAMFNPAPYLPSCLE 23

Scoring table: BIOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	123	100.0	448	WT1_RAT	P49952 ratu nov
2	123	100.0	449	WT1_HUMAN	P19544 homo sapien
3	123	100.0	449	WT1_MOUSE	P22561 mus musculu
4	123	100.0	449	WT1_PIG	O62651 sus scrofa
5	52	42.3	82	9KD_HUMAN	P13994 homo sapien
6	49	39.8	885	YD03_YEAST	O06639 saccharomyc
7	48	39.0	618	IAP2_HUMAN	Q13490 homo sapien
8	47	38.2	271	IBP5_MOUSE	O07079 mus musculu
9	47	38.2	271	IBP5_PIG	Q28985 sus scrofa
10	47	38.2	271	IBP5_RAT	P24594 ratu nov
11	47	38.2	272	IBP5_HUMAN	P24593 homo sapien
12	46	37.4	545	SYK_STRCO	O9X895 streptomyc
13	46	37.4	556	GLI_CHICK	P55678 gallus gall
14	45	36.6	382	KSEL_ECOLI	P42501 escherichia
15	45	36.6	382	KSEL_ECOLI	P42514 escherichia
16	45	36.6	537	KSE5_ECOLI	O18635 musca domes
17	44	35.8	726	NU5M_MUSDO	P41309 didelphis m
18	44	35.8	726	NE11_YEAST	Q12316 saccharomyc
19	44	35.8	738	TREX_HUMAN	P08582 homo sapien
20	43.5	35.4	188	CR12_HUMAN	P13385 homo sapien
21	43.5	35.4	188	CR12_HUMAN	P51664 homo sapien
22	43.5	35.4	337	G3P_METFE	P10618 methanococ
23	43	35.0	91	DEFX_MOUSE	O64263 mus musculu
24	43	35.0	118	YTON_ENTAE	P46381 enterobacte
25	43	35.0	353	TPO_HUMAN	P40225 homo sapien
26	43	35.0	526	BGP1_HUMAN	P13688 homo sapien
27	43	35.0	594	NU5M_HIPAM	O92971 hippopotanu
28	43	35.0	601	NU5M_DASNO	O21353 dasypus nov
29	43	35.0	602	NU5M_MACRO	P92669 macropus ro
30	43	35.0	603	NU5M_RABIT	P79437 oryctolagus
31	43	35.0	604	NU5M_HORSE	P48656 equus cabal
32	43	35.0	606	NU5M_BALMU	P41299 balaenopter
33	43	35.0	606	NU5M_BALPH	P24978 balaenopter

34	43	35.0	606	1	NU5M_BOVIN	P03920 bos taurus
35	43	35.0	606	1	NU5M_CANFA	O92577 canis fam11
36	43	35.0	606	1	NU5M_CERSI	O03205 ceratotheri
37	43	35.0	606	1	NU5M_EOUAS	P92485 equus asinu
38	43	35.0	606	1	NU5M_FELCA	P48921 felis silve
39	43	35.0	606	1	NU5M_RHION	O96069 rhinoceros
40	43	35.0	606	1	NU5M_SHEEP	O78766 ovis aries
41	43	35.0	607	1	NU5M_CARAU	O78688 carassius a
42	43	35.0	607	1	NU5M_MOUSE	P03921 mus musculu
43	43	35.0	609	1	NU5M_HALCR	P38602 halichoerus
44	43	35.0	609	1	NU5M_PHOVI	O00542 phoca vitul
45	43	35.0	609	1	NU5M_SCVCA	O79411 scyllorhinu

## ALIGNMENTS

RESULT	1	WT1_RAT	STANDARD	PRT	448 AA
WT1_RAT	AC	P49952			
WT1_RAT	DT	01-OCT-1996 (Rel. 34, Created)			
WT1_RAT	DT	01-OCT-1996 (Rel. 34, Last sequence update)			
WT1_RAT	DT	01-OCT-2000 (Rel. 40, Last annotation update)			
WT1_RAT	DE	WILMS' TUMOR PROTEIN HOMOLOG.			
WT1_RAT	GN	WT1 OR WT-1.			
WT1_RAT	OS	Rattus norvegicus (Rat).			
WT1_RAT	OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
WT1_RAT	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.			
WT1_RAT	RN	[1]			
WT1_RAT	RP	SEQUENCE FROM N.A.			
WT1_RAT	RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=KIDNEY;			
WT1_RAT	RA	MEDLINE=93046155; PubMed=1350293;			
WT1_RAT	RX	Sharma P.M., Yang X., Bowman M., Roberts V., Sukumar S.;			
WT1_RAT	RT	"Molecular cloning of rat Wilms' tumor complementary DNA and a study			
WT1_RAT	RT	of messenger RNA expression in the urogenital system and the brain."			
WT1_RAT	RL	Cancer Res. 52:6407-6412(1992)			
WT1_RAT	CC	-1- FUNCTION: POTENTIAL ROLE IN TRANSCRIPTIONAL REGULATION. RECOGNIZES			
WT1_RAT	CC	AND BINDS TO THE DNA SEQUENCE 5'-GGCCCCGC-3'.			
WT1_RAT	CC	-1- SUBCELLULAR LOCATION: NUCLEAR.			
WT1_RAT	CC	-1- ALTERNATIVE PRODUCTS: TWO ALTERNATIVE SPLICING SITES EXISTS.			
WT1_RAT	CC	-1- TISSUE SPECIFICITY: KIDNEY (BY SIMILARITY).			
WT1_RAT	CC	-1- DEVELOPMENTAL STAGE: EXPRESSED DURING KIDNEY DEVELOPMENT.			
WT1_RAT	CC	-1- SIMILARITY: BELONGS TO THE EGR FAMILY OF C/2H2-TYPE ZINC-FINGER			
WT1_RAT	CC	PROTEINS.			
WT1_RAT	CC	-----			
WT1_RAT	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
WT1_RAT	CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -			
WT1_RAT	CC	the European Bioinformatics Institute. There are no restrictions on its			
WT1_RAT	CC	use by non-profit institutions as long as its content is in no way			
WT1_RAT	CC	modified and this statement is not removed. Usage by and for commercial			
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WT1_RAT	CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
WT1_RAT	CC	-----			
WT1_RAT	CC	EMBL: X69716; CAA49373.1; -			
WT1_RAT	CC	TRANSFAC: T02352; -			
WT1_RAT	CC	INTERPRO: IPR000822; -			
WT1_RAT	CC	DR INTERPRO: IPR000976; -			
WT1_RAT	CC	PFAM: PF00096; ZF-C2H2; 4.			
WT1_RAT	CC	PRINTS: PR00048; ZINC-FINGER.			
WT1_RAT	CC	PRINTS: PR00049; WILMS-TUMOR.			
WT1_RAT	CC	PROSITE: PS00028; ZINC-FINGER C2H2; 4.			
WT1_RAT	CC	Zinc-finger; Metal-binding; DNA-binding; Repeat; Nuclear protein;			
WT1_RAT	CC	Transcription regulation; Alternative splicing; Anti-oncogene.			
WT1_RAT	CC	-----			
WT1_RAT	CC	DOMAIN 27 82			
WT1_RAT	CC	FT DOMAIN 322 437			
WT1_RAT	CC	FT ZN_FING 322 437			
WT1_RAT	CC	FT ZN_FING 322 437			
WT1_RAT	CC	FT ZN_FING 352 376			
WT1_RAT	CC	FT ZN_FING 382 404			
WT1_RAT	CC	FT ZN_FING 413 437			
WT1_RAT	CC	FT ZN_FING 429 265			
WT1_RAT	CC	FT VARSPLIC 247 409			
WT1_RAT	CC	FT VARSPLIC 448 AA; 49193 MW; 329AC9AC1F73E76 CFC64;			
WT1_RAT	CC	MISSING (IN ISOFORM 2 AND ISOFORM 3).			
WT1_RAT	CC	MISSING (IN ISOFORM 2 AND ISOFORM 4).			
WT1_RAT	CC	SEQUENCE			

Query Match 100.0%; Score 123; DB 1; Length 448;  
 Best Local Similarity 100.0%; Pred. No. 1,4e-11;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 1 PSQASSGQARMFPNAPVLPSCLE 23  
 |||||||||||||||||||  
 Db 116 PSQASSGQARMFPNAPVLPSCLE 138

RESULT 2  
 ID WT1\_HUMAN STANDARD; PRT; 449 AA.  
 AC P19544;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE WILMS' TUMOR PROTEIN (WT33).  
 GN WT1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=FETAL KIDNEY;  
 RX MEDLINE=90158822; PubMed=2154702;  
 RA Gessler M., Poustka A., Cavenee W., Neve R.L., Orkin S.H.,  
 RT Bruns G.A.P.;  
 RT "Homozygous deletion in Wilms tumours of a zinc-finger gene  
 RT identified by chromosome jumping.";  
 RL Nature 343:774-778(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PLACENTA;  
 RX MEDLINE=92052142; PubMed=1658787;  
 RA Haber D.A., Sohn R.L., Buckler A.J., Pelletier J., Call K.M.,  
 RT Housman D.E.;  
 RT "Alternative splicing and genomic structure of the Wilms tumor gene  
 RT WT1.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:9618-9622(1991).  
 RN [3]  
 RP SEQUENCE OF 85-449 FROM N.A.  
 RC MEDLINE=90150277; PubMed=2154335;  
 RX Call K.M., Glaser T., Ito C.Y., Buckler A.J., Pelletier J.,  
 RA Haber D.A., Rose E.A., Kral A., Yeager H., Lewis W.H., Jones C.,  
 RT Housman D.E.;  
 RT "Isolation and characterization of a zinc finger polypeptide gene at  
 RT the human chromosome 11 Wilms' tumor locus.";  
 RL Cell 60:509-520(1990).  
 RN [4]  
 RP IDENTIFICATION OF START CODON AND ALTERNATIVE SPLICE SITES.  
 RC MEDLINE=91141522; PubMed=1671709;  
 RX Buckler A.J., Pelletier J., Haber D.A., Glaser T., Housman D.E.;  
 RT "Isolation, characterization, and expression of the murine Wilms'  
 RT tumor gene (WT1) during kidney development.";  
 RL Mol. Cell. Biol. 11:1707-1712(1991).  
 RN [5]  
 RP VARIANT WT CYS-366.  
 RC MEDLINE=92279213; PubMed=1317572;  
 RX Little M.H., Prosser J., Condie A., Smith P.J., van Heyningen V.,  
 RA Hastie N.D.;  
 RT "Zinc finger point mutations within the WT1 gene in Wilms tumor  
 RT patients.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:4791-4795(1992).  
 RN [6]  
 RP VARIANTS DDS.  
 RC MEDLINE=92005721; PubMed=1655284;  
 RX Pelletier J., Breuning W., Kashtan C.E., Mauer S.M., Manivel J.C.,  
 RA Striegler J.E., Houghton D.C., Jundt C., Habib R., Fouser L.,  
 RA Fine R.N., Silverman B.L., Haber D.A., Housman D.;  
 RT "Germline mutations in the Wilms' tumor suppressor gene are  
 RT associated with abnormal urogenital development in Denys-Drash

RT syndrome.";  
 RL Cell 67:437-447(1991).  
 RN [7]  
 RP VARIANTS DDS.  
 RC MEDLINE=93265053; PubMed=1338906;  
 RX Baird P.N., Santos A., Groves N., Jadresic L., Cowell J.K.;  
 RT "Constitutional mutations in the WT1 gene in patients with  
 RT Denys-Drash syndrome.";  
 RL Hum. Mol. Genet. 1:301-305(1992).  
 RN [8]  
 RP VARIANTS DDS.  
 RC MEDLINE=93271983; PubMed=8388765;  
 RX Little M.H., Williamson K.A., Mannens M., Kelsey A., Gosden C.,  
 RA Hastie N., van Heyningen V.;  
 RT "Evidence that WT1 mutations in Denys-Drash syndrome patients may act  
 RT in a dominant-negative fashion.";  
 RL Hum. Mol. Genet. 2:259-264(1993).  
 RN [9]  
 RP VARIANT MESOTHELIOMA GLX-273.  
 RC MEDLINE=94004972; PubMed=8401592;  
 RX Park S., Schalling M., Bernard A., Maheswaran S., Shipley G.C.,  
 RA Roberts D., Fletcher J., Shipman R., Rheinwald J., Demetri G.,  
 RA Griffin J., Minden M., Housman D.E., Haber D.A.;  
 RT "The Wilms tumor gene WT1 is expressed in murine mesoderm-derived  
 RT tissues and mutated in a human mesothelioma.";  
 RL Nat. Genet. 4:415-420(1993).  
 RN [10]  
 RP VARIANTS WT SER-181 AND ALA-253.  
 RC MEDLINE=97268681; PubMed=9108089;  
 RX Schmacher V., Schneider S., Fluge A., Wildhardt G., Harms D.,  
 RA Schmidt D., Weirich A., Ludwig R., Royer-Pokora B.;  
 RT "Correlation of germ-line mutations and two-hit inactivation of the  
 RT WT1 gene with Wilms tumors of stromal-predominant histology.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:3972-3977(1997).  
 RN [11]  
 RP VARIANTS DMS TYR-377; LEU-383 AND ASN-396.  
 RC MEDLINE=98198341; PubMed=9529364;  
 RX Jeanpierre C., Denamur E., Henry I., Cabanis M.-O., Luce S.,  
 RA Cecille A., Elion J., Peuchmaur M., Lorlat C., Maudet P.,  
 RA Gubler M.-C., Jundt C.;  
 RT "Identification of constitutional WT1 mutations in patients with  
 RT isolated diffuse mesangial sclerosis, and analysis of  
 RT genotype/phenotype correlations by use of a computerized mutation  
 RT database.";  
 RL Am. J. Hum. Genet. 62:824-833(1998).  
 RN [12]  
 RP REVIEW.  
 RC MEDLINE=92207913; PubMed=1313285;  
 RX Haber D.A., Buckler A.J.;  
 RT "WT1: a novel tumor suppressor gene inactivated in Wilms' tumor.";  
 RL New Biol. 4:97-106(1992).  
 RN [13]  
 RP REVIEW.  
 RC MEDLINE=93345769; PubMed=8393820;  
 RX Rauscher F.J. III;  
 RT "The WT1 Wilms tumor gene product: a developmentally regulated  
 RT transcription factor in the kidney that functions as a tumor  
 RT suppressor.";  
 RL FASEB J. 7:896-903(1993).  
 CC -1- FUNCTION: POTENTIAL ROLE IN TRANSCRIPTIONAL REGULATION. RECOGNIZES  
 CC AND BINDS TO THE DNA SEQUENCE 5'-CGCCCCCGC-3'.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.  
 CC -1- ALTERNATIVE PRODUCTS: TWO ALTERNATIVE SPLICE SITES EXISTS.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE KIDNEY AND A SUBSET OF  
 CC HEMATOPOIETIC CELLS.  
 CC -1- DISEASE: WILMS TUMOR (WT) IS AN EMBRYONAL MALIGNANCY OF THE  
 CC KIDNEY THAT AFFECTS APPROXIMATELY 1 IN 10,000 INFANTS AND YOUNG  
 CC CHILDREN. IT OCCURS BOTH IN SPORADIC AND HEREDITARY FORMS.  
 CC INACTIVATION OF WT1 IS ONE OF THE CAUSES OF WILMS TUMOR.  
 CC -1- DISEASE: PATIENTS WITH DENYS-DRASH SYNDROME (DDS), WHICH IS  
 CC CHARACTERIZED BY A TYPICAL NEPHROPATHY AND GENITAL ABNORMALITIES,  
 CC HAVE DEFECTS IN THE WT1 GENE.  
 CC -1- DISEASE: DEFECTS IN WT1 ARE ALSO A CAUSE OF DIFFUSE MESANGIAL



CC SCIEROSIS (DMS), A FORM A DDS.  
 CC -1- SIMILARITY: BELONGS TO THE EGR FAMILY OF C2H2-TYPE ZINC-FINGER  
 CC PROTEINS.  
 CC -1- DATABASE: NAME=WT1; NOTE=WT1 mutation database;  
 CC WWW="http://www.umd.necker.fr:2003/".  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----  
 CC EMBL: X51630; CAA59596.1; ALT\_INIT.  
 CC DR EMBL: M80232; AAA61299.1; -.  
 CC DR EMBL: M80217; AAA61299.1; JOINED.  
 CC DR EMBL: M80218; AAA61299.1; JOINED.  
 CC DR EMBL: M80219; AAA61299.1; JOINED.  
 CC DR EMBL: M80220; AAA61299.1; JOINED.  
 CC DR EMBL: M80221; AAA61299.1; JOINED.  
 CC DR EMBL: M80228; AAA61299.1; JOINED.  
 CC DR EMBL: M80229; AAA61299.1; JOINED.  
 CC DR EMBL: M80231; AAA61299.1; JOINED.  
 CC DR EMBL: M30393; AAA36810.1; -.  
 CC DR PIR: A34673; A34673.  
 CC DR PIR: S08273; S08273.  
 CC DR TRANSFAC: T00899; -.  
 CC DR MIM: 194070; -.  
 CC DR MIM: 194080; -.  
 CC DR MIM: 256370; -.  
 CC DR INTERPRO: IPR000822; -.  
 CC DR INTERPRO: IPR000976; -.  
 CC DR PEAM: PF000096; zf-C2H2; 4.  
 CC DR PRINTS: PR00048; ZINC\_FINGER.  
 CC DR PRINTS: PR00049; WILMSTUMOUR.  
 CC DR PROSITE: PS00028; ZINC\_FINGER\_C2H2; 4.  
 CC DR Zinc-finger; Metal-binding; Repeat; Nuclear protein;  
 CC transcription regulation; Alternative splicing; Anti-oncogene;  
 CC disease mutation.  
 CC -----  
 CC FT DOMAIN 27 83 PRO-RICH.  
 CC FT ZN\_FING 323 438 ZINC FINGERS.  
 CC FT ZN\_FING 323 347 C2H2-TYPE.  
 CC FT ZN\_FING 353 377 C2H2-TYPE.  
 CC FT ZN\_FING 383 405 C2H2-TYPE.  
 CC FT ZN\_FING 414 438 C2H2-TYPE.  
 CC FT VARSPLIC 250 266 MISSING (IN ISOFORM 2 AND ISOFORM 3).  
 CC FT VARSPLIC 408 410 MISSING (IN ISOFORM 2 AND ISOFORM 4).  
 CC FT VARSPLIC 181 181 P -> S (IN WT).  
 CC FT VARIANT 223 223 /FTID=VAR\_007739.  
 CC FT VARIANT 223 223 S -> N (IN WT).  
 CC FT VARIANT 253 253 /FTID=VAR\_007740.  
 CC FT VARIANT 253 253 G -> A (IN WT).  
 CC FT VARIANT 273 273 /FTID=VAR\_007741.  
 CC FT VARIANT 273 273 S -> G (IN MESOTHELIOMA).  
 CC FT VARIANT 330 330 /FTID=VAR\_007742.  
 CC FT VARIANT 330 330 C -> Y (IN DDS).  
 CC FT VARIANT 360 360 /FTID=VAR\_007743.  
 CC FT VARIANT 360 360 C -> G (IN DDS).  
 CC FT VARIANT 366 366 /FTID=VAR\_007744.  
 CC FT VARIANT 366 366 R -> C (IN WT).  
 CC FT VARIANT 366 366 /FTID=VAR\_007745.  
 CC FT VARIANT 366 366 R -> H (IN DDS).  
 CC FT VARIANT 373 373 /FTID=VAR\_007746.  
 CC FT VARIANT 373 373 H -> Q (IN DDS).  
 CC FT VARIANT 377 377 /FTID=VAR\_007747.  
 CC FT VARIANT 377 377 H -> Y (IN DDS/DMS).  
 CC -----  
 CC Query Match 100.0%; Score 123; DB 1; Length 449;  
 CC Best Local Similarity 100.0%; Pred. No. 1.4e-11;  
 CC Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 117 PSQASSGOARMPNAPYLPSCLE 139  
 RESULT 3  
 WT1\_MOUSE STANDARD; PRT: 449 AA.  
 AC P22561;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE WILMS' TUMOR PROTEIN HOMOLOG.  
 GN WT1 OR WT-1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91141522; PubMed=1671709;  
 RA Buckler A.J., Pelletier J., Haber D.A., Glaser T., Housman D.E.;  
 RT "Isolation, characterization, and expression of the murine Wilms'  
 RT tumor gene (WT1) during kidney development.";  
 RL Mol. Cell. Biol. 11:1707-1712(1991).  
 CC -1- FUNCTION: POTENTIAL ROLE IN TRANSCRIPTIONAL REGULATION. RECOGNIZES  
 CC AND BINDS TO THE DNA SEQUENCE 5'-GGCCCCCG-3'.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.  
 CC -1- ALTERNATIVE PRODUCTS: TWO ALTERNATIVE SPLICE SITES EXISTS.  
 CC -1- TISSUE SPECIFICITY: KIDNEY.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING KIDNEY DEVELOPMENT.  
 CC -1- SIMILARITY: BELONGS TO THE EGR FAMILY OF C2H2-TYPE ZINC-FINGER  
 CC PROTEINS.  
 CC -----  
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 CC -----  
 CC EMBL: M55512; AAA40573.1; -.  
 CC DR PIR: A39692; A39692.  
 CC DR TRANSFAC: T02351; -.  
 CC DR MGD: MGI:98968; WT1.  
 CC DR INTERPRO: IPR000822; -.  
 CC DR INTERPRO: IPR000976; -.  
 CC DR PEAM: PF000096; zf-C2H2; 4.  
 CC DR PRINTS: PR00048; ZINC\_FINGER.  
 CC DR PRINTS: PR00049; WILMSTUMOUR.  
 CC DR PROSITE: PS00028; ZINC\_FINGER\_C2H2; 4.  
 CC DR Zinc-finger; Metal-binding; DNA-binding; Repeat; Nuclear protein;  
 CC transcription regulation; Alternative splicing; Anti-oncogene.  
 CC -----  
 CC FT DOMAIN 28 83 PRO-RICH.  
 CC FT ZN\_FING 323 438 ZINC FINGERS.  
 CC FT ZN\_FING 323 347 C2H2-TYPE.  
 CC FT ZN\_FING 353 377 C2H2-TYPE.  
 CC FT ZN\_FING 383 405 C2H2-TYPE.  
 CC FT ZN\_FING 414 438 C2H2-TYPE.  
 CC FT VARSPLIC 250 266 MISSING (IN ISOFORM 2 AND ISOFORM 3).  
 CC FT VARSPLIC 408 410 MISSING (IN ISOFORM 2 AND ISOFORM 4).  
 CC FT VARSPLIC 962381E9C8D7A380 CRC64;  
 CC FT SEQUENCE 449 AA; 49246 MW; 962381E9C8D7A380 CRC64;  
 CC -----  
 CC Query Match 100.0%; Score 123; DB 1; Length 449;  
 CC Best Local Similarity 100.0%; Pred. No. 1.4e-11;  
 CC Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PSQASSGOARMPNAPYLPSCLE 23  
 Db 117 PSQASSGOARMPNAPYLPSCLE 139  
 RESULT 4

WT1\_PIG STANDARD: PRT: 449 AA.  
 AC 062651.  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE WILMS' TUMOR PROTEIN HOMOLOG.  
 GN WT1.  
 OS Sus scrofa (Pig)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LMD: TISSUE-KIDNEY;  
 RX MEDLINE=98267201; PubMed=9602131;  
 RA Tsutsumi N., Oda H., Nakatsuru Y., Imai Y., Zhang S., Ueno Y.,  
 RA Ishikawa T.;  
 RT "CDNA cloning and developmental expression of the porcine homologue  
 of WT1.";  
 RT Gene 211:215-220(1998).  
 CC -1- FUNCTION: POTENTIAL ROLE IN TRANSCRIPTIONAL REGULATION. RECOGNIZES  
 CC AND BINDS TO THE DNA SEQUENCE 5'-GGCCCCGC-3'.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.  
 CC -1- ALTERNATIVE PRODUCTS: TWO ALTERNATIVE SPLICE SITES EXISTS.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING KIDNEY DEVELOPMENT.  
 CC -1- SIMILARITY: BELONGS TO THE EGR FAMILY OF C2H2-TYPE ZINC-FINGER  
 CC PROTEINS.  
 CC -----  
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 CC -----  
 DR EMBL: AB010969; BAA28147.1; -  
 DR INTERPRO: IPR000822; -  
 DR INTERPRO: IPR000976; -  
 DR Pfam: PF00096; zf-C2H2; 4.  
 DR PRINTS: PR00048; ZINC\_FINGER.  
 DR PRINTS: PR00049; WILMS\_TUMOR.  
 DR PROSITE: PS00028; ZINC\_FINGER\_C2H2; 4.  
 DR Zinc-finger; Metal-binding; DNA-binding; Repeat; Nuclear protein;  
 DR Transcription regulation; Alternative splicing; Anti-oncogene.  
 FT DOMAIN 28 PRO-RICH.  
 FT 323 438 ZINC FINGERS.  
 FT 323 347 C2H2-TYPE.  
 FT 323 377 C2H2-TYPE.  
 FT 353 377 C2H2-TYPE.  
 FT 383 405 C2H2-TYPE.  
 FT 414 438 C2H2-TYPE.  
 FT 249 265 MISSING (IN ISOFORM 2 AND ISOFORM 3) (BY  
 FT SIMILARITY).  
 FT VARSPLIC 407 409 MISSING (IN ISOFORM 2 AND ISOFORM 4) (BY  
 FT SIMILARITY).  
 SQ SEQUENCE 449 AA; 49166 MW; 9C3E557B96F5A7B3 CRC64;

DT 01-JAN-1990 (Rel. 13, Last annotation update)  
 DE 9 KDA PROTEIN.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-FIBROBLAST;  
 RX MEDLINE=89078418; PubMed=3203696;  
 RA Lammers R., Gross G., Mayr U., Collins J.;  
 RT "Alternative mechanisms for gene activation induced by  
 RT poly(rl).poly(rc) and Newcastle disease virus.";  
 RT Eur. J. Biochem. 178:93-99(1988).  
 CC -1- INDUCTION: BY POLY(rl), POLY(rc) AND NEWCASTLE DISEASE VIRUS.  
 CC -----  
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 CC -----  
 DR EMBL: X13956; CAA32138.1; -  
 DR PIR: S02660; S02660.  
 SQ SEQUENCE 82 AA; 8594 MW; 9B4A1552A489652 CRC64;

Query Match 42.3%; Score 52; DB 1; Length 82;  
 Best Local Similarity 47.8%; Pred. No. 0.19;  
 Matches 11; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

OY 1 PSQASSGOARMPNAPYLPSCLE 23  
 I : I I I : I I I I I : I I I  
 DB 23 PLEASSTRARFPCPLVACEPE 45

RESULT 6  
 YD03\_YEAST STANDARD: PRT: 885 AA.  
 AC 006639;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE PUTATIVE 101.7 KDA TRANSCRIPTIONAL REGULATORY PROTEIN IN PROI-CPRS  
 DE INTERGENIC REGION.  
 GN YDR303C OR D9740.13.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;  
 OC Saccharomycetaceae; Saccharomyces.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=5288C / AB972;  
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,  
 RA Faveille A., Fulton L., Gattung S., Greco T., Kirsten J.,  
 RA Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,  
 RA Johnson D., Johnston L., Langston Y., Latreille P., Le T.,  
 RA Mardis E., Meneses S., Miller N., Nhan M., Pauley A., Peluso D.,  
 RA Rifken L., Riles L., Tach A., Trevisan E., Vignati D.,  
 RA Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R.;  
 RT Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).  
 CC -1- SIMILARITY: CONTAINS A ZN(2)-CYS(6), FUNGAL-TYPE BINUCLEAR  
 CC CLUSTER DOMAIN.  
 CC -----  
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 CC -----



Query Match	38.2%	Score 47	DB 1	Length 271
Best Local Similarity	47.4%	Pred. No. 3.8		
Matches 9	Conservative 1	Mismatches 9	Indels 0	Gaps 0
QY	3 QASSGQARMPNPAPYLPSG 21			
Db	200 QEFKASPRMYPRAVYLPNC 218			
RESULT	9			
IBP5_PIG				
IBP5_PIG	STANDARD	PRT	271	AA
AC	028985			
DT	01-NOV-1997 (Rel. 35, Created)			

Query Match	38.2%	Score 47	DB 1	Length 271
Best Local Similarity	47.4%	Pred. No. 3.8		
Matches	9	Conservative	1	Mismatches 9
				Indels 0
				Gaps 0
QY	3 QASSGQARMPENAPVLPSC 21			
Db	200 QELKASPRMVPRAVYLPMC 218			
RESULT 10				
IBP5_RAT		STANDARD	PRT	271 AA.
1D	IBP5_RAT			
AC	P24594			
DT	01-MAR-1992 (Rel. 21, Created)			
DT	01-MAR-1992 (Rel. 21, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 5 PRECURSOR (IGFBP-5)			
DE	(IBP-5) (IGF-BINDING PROTEIN 5).			
GN	IGFBP5 OR IGFBP-5.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
NP	[1]			
	SEQUENCE FROM N. A., AND SEQUENCE OF 20-53.			





DT 01-NOV-1995 (rel. 32, Created)  
 DT 01-NOV-1995 (rel. 32, Last sequence update)  
 DT 01-FEB-1996 (rel. 33, Last annotation update)  
 DE CAPSULE POLYSACCHARIDE EXPORT INNER-MEMBRANE PROTEIN KPSE.  
 GN KPSE.  
 OS Escherichia coli.  
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 CC Escherichia.  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K1;  
 RX MEDLINE=94075243; PubMed=8253690;  
 RA Cieslewicz M.D., Steenbergen S.M., Vint E.R.;  
 RT Cloning, sequencing, expression, and complementation analysis of the  
 RT Escherichia coli K1 kps region 1 gene, kpse, and identification of an  
 RT upstream open reading frame encoding a protein with homology to  
 RT Guto."  
 RL J. Bacteriol. 175:8018-8023(1993).  
 CC -1- FUNCTION: INVOLVED IN THE TRANSLLOCATION OF THE POLYSTALIC ACID  
 CC CAPSULE.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE  
 CC (POTENTIAL).  
 CC -1- SIMILARITY: BELONGS TO THE BEXC/CTRB/KPSE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: L19929; AAB51624.1; ALT\_INIT.  
 DR POLYSACCHARIDE transport; Transport; Transmembrane; Inner membrane.  
 FT TRANSMEM 28 48 POTENTIAL.  
 FT TRANSMEM 357 377 POTENTIAL.  
 SQ SEQUENCE 382 AA; 43049 MW; 05D25E12BD86F4B5 CRC64;

Query Match 36.6%; Score 45; DB 1; Length 382;  
 Best Local Similarity 57.1%; Pred. No. 11;  
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 8 QARMPNAPYLPSC 21  
 DB 345 QESSFPNIPYLAC 358

RESULT 15  
 KSES\_ECOLI STANDARD; PRT; 382 AA.  
 AC P42214;  
 DT 01-NOV-1995 (rel. 32, Created)  
 DT 01-NOV-1995 (rel. 32, Last sequence update)  
 DT 01-NOV-1995 (rel. 32, Last annotation update)  
 DE CAPSULE POLYSACCHARIDE EXPORT INNER-MEMBRANE PROTEIN KPSE.  
 GN KPSE.  
 OS Escherichia coli.  
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 CC Escherichia.  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K5;  
 RX MEDLINE=93388530; PubMed=8397187;  
 RA Pazhani C., Rosenow C., Boulnois G.J., Bronner D., Jann K.,  
 RA Roberts I.S.;  
 RT Molecular analysis of region 1 of the Escherichia coli K5 antigen  
 RT gene cluster: a region encoding proteins involved in cell surface  
 RT expression of capsular polysaccharide."  
 RL J. Bacteriol. 175:5978-5983(1993).  
 CC -1- FUNCTION: INVOLVED IN THE TRANSLLOCATION OF THE POLYSTALIC ACID  
 CC CAPSULE.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE

CC (POTENTIAL).  
 CC -1- SIMILARITY: BELONGS TO THE BEXC/CTRB/KPSE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: X74567; CA52655.1;  
 DR POLYSACCHARIDE transport; Transport; Transmembrane; Inner membrane.  
 FT TRANSMEM 28 48 POTENTIAL.  
 FT TRANSMEM 357 377 POTENTIAL.  
 SQ SEQUENCE 382 AA; 43044 MW; 44E9508484DC05B2 CRC64;

Query Match 36.6%; Score 45; DB 1; Length 382;  
 Best Local Similarity 57.1%; Pred. No. 11;  
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 8 QARMPNAPYLPSC 21  
 DB 345 QESSFPNIPYLAC 358

Search completed: April 11, 2001, 14:03:53  
 Job time: 114 sec

0.0



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: April 11, 2001, 13:53:45 ; Search time 14.03 Seconds

(without alignments)  
111.313 Million cell updates/sec

Title: US-09-164-223-2

Perfect score: 123

Sequence: 1 PSQASSGQARMFPNAPLPSCLE 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq Length: 0

Maximum DB seq Length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 66:\*

2: PIR1:\*

3: PIR2:\*

4: PIR3:\*

#### SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	123	100.0	448	2	S33926
2	123	100.0	449	2	A38080
3	123	100.0	449	2	A39692
4	103	83.7	410	2	JC5046
5	52	42.3	82	2	S02660
6	49	39.8	634	2	E82999
7	49	39.8	885	2	S61189
8	48	39.0	188	2	T79500
9	48	39.0	188	2	JU0451
10	48	39.0	188	2	T59116
11	48	39.0	188	2	A29867
12	48	39.0	600	2	D83286
13	48	39.0	618	2	S68450
14	48	39.0	778	2	T17679
15	47	38.2	271	2	JC4584
16	47	38.2	271	2	I48604
17	47	38.2	271	2	JC1463
18	47	38.2	815	2	A53748
19	47	38.2	815	2	B30843
20	47	38.2	815	2	JN0689
21	46	37.4	830	2	S15720
22	46	37.4	545	2	T36123
23	46	37.4	606	2	T45560
24	46	37.4	955	2	T00247
25	45.5	37.0	704	2	T24517
26	45	36.6	381	2	A54415
27	45	36.6	382	2	A48492
28	45	36.6	484	2	JC7350
29	45	36.6	488	2	T33739

30	44	35.8	292	2	G64695	conserved hypothet
31	44	35.8	292	2	A71824	probable ribonucle
32	44	35.8	376	2	T46097	hypothetical prote
33	44	35.8	393	2	T20268	hypothetical prote
34	44	35.8	449	2	JC5117	translational elonga
35	44	35.8	472	2	T04855	hypothetical prote
36	44	35.8	590	2	T11098	NADH dehydrogenase
37	44	35.8	602	2	S47680	probable outer mem
38	44	35.8	615	2	A82025	NEIL protein - yea
39	44	35.8	726	2	S67044	melanotransferrin
40	44	35.8	738	1	TFH0M	hypothetical prote
41	44	35.8	1286	2	B71413	epidermal growth f
42	43.5	35.4	188	2	A39787	epidermal growth f
43	43.5	35.4	188	2	A30362	glyceraldhyde-3-P
44	43.5	35.4	337	1	JT0286	DNA-directed DNA p
45	43.5	35.4	832	2	S67505	

#### ALIGNMENTS

RESULT 1  
S33926  
WILMS' tumor protein WT1 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 10-May-1996  
C:Accession: S33926  
R:Sharma, P.M., Yang, X.; Bowman, M.; Roberts, V.; Sukumar, S.  
Cancer Res. 52, 6407-6412, 1992  
A:Title: Molecular cloning of rat WILMS' tumor complementary DNA and a study of messe  
A:Reference number: S33926; MUID:93046155  
A:Accession: S33926  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-448 <SHA>  
A:Cross-references: EMBL:X69716  
C:Genetics:  
A:Gene: WT1  
C:Keywords: tumor suppressor

Query Match 100.0%; Score 123; DB 2; Length 448;  
Best Local Similarity 100.0%; Pred. No. 2.4e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PSQASSGQARMFPNAPLPSCLE 23  
DB 116 PSQASSGQARMFPNAPLPSCLE 138  
RESULT 2  
A38080  
WILMS tumor susceptibility protein WT1 - human  
C:Species: Homo sapiens (man)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 20-Jun-2000  
C:Accession: A38080; S08273; A34673; I38504; I52811; I56315; A56411; S26286  
R:Gessler, M.; Konig, A.; Bruns, G.A.  
Genomics 12, 807-813, 1992  
A:Title: The genomic organization and expression of the WT1 gene.  
A:Reference number: A38080; MUID:92241883  
A:Accession: A38080  
A:Molecule type: DNA  
A:Residues: 1-449 <GES1>  
A:Cross-references: GB:X61631; GB:S99414; NID:937981; PIDN:CAA43819.1; PID:9825731  
A>Note: it is uncertain whether Met-1 is the initiator or whether translation is init  
A>Note: Sequence extracted from NCBI backbone (NCBIN:99414; NCBIN:99422; NCBIN:99479,  
R:Gessler, M.; Poustka, A.; Cavenee, W.; Neve, R.L.; Orkin, S.H.; Bruns, G.A.P.  
Nature 343, 774-778, 1990  
A:Title: Homozygous deletion in WILMS tumours of a zinc-finger gene identified by chr  
A:Reference number: S08273; MUID:90158822  
A:Accession: S08273  
A:Molecule type: mRNA

A:Residues: 'SRORPHGALRNPTACLPHPSPSPPTHPHPRAGTAACAPCPRLAALIDPLLLIDDPASTCVPEPASQHT  
 A:Cross-references: EMBL:X51630; NID:q37977; PID:CA35956.1; PID:q37978  
 R:Call, K.M.; Glaser, T.; Ito, C.Y.; Buckler, A.J.; Pelletier, J.; Haber, D.A.; Rose, E.  
 Cell 60, 509-520, 1990  
 A:Title: Isolation and characterization of a zinc finger polypeptide gene at the human c  
 A:Reference number: A34673; MUID:90150277  
 A:Accession: A34673  
 A:Molecule type: mRNA  
 A:Residues: 85-249,267-364,'F',366-386,'T',388-407,411-449 <CAL>  
 A:Cross-references: GB:M30393; NID:q340381; PID:AAA62865.1; PID:q458432  
 R:Haber, D.A.; Sohn, R.L.; Buckler, A.J.; Pelletier, J.; Call, K.M.; Housman, D.E.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 9618-9622, 1991  
 A:Title: Alternative splicing and genomic structure of the Wt1ms tumor gene Wt1.  
 A:Reference number: A56411; MUID:92052142  
 A:Contents: annotation: alternative splicing  
 R:Phelan, S.A.; Lindberg, C.; Call, K.M.  
 Cell Growth Differ. 5, 677-686, 1994  
 A:Title: Wt1ms' tumor gene, Wt1, mRNA is down-regulated during induction of erythroid an  
 A:Reference number: I38504; MUID:94368704  
 A:Accession: I38504  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-18 <PHE>  
 A:Cross-references: EMBL:U06486; NID:q473563; PID:AAA62865.1; PID:q458432  
 R:Pelletier, J.; Bruening, W.; Kashlan, C.E.; Mauer, S.M.; Manivel, J.C.; Striegel, J.E.  
 Cell 67, 437-447, 1991  
 A:Title: Germ-line mutations in the Wt1ms' tumor suppressor gene are associated with abno  
 A:Reference number: I52811; MUID:92005721  
 A:Accession: I52811  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 355-365,'H',367-377 <PEL>  
 A:Cross-references: GB:S61513; NID:q337599; PID:AAA20109.1; PID:q237600  
 A:Note: mutant form  
 R:Hamilton, T.B.; Barilla, K.C.; Romanik, P.J.  
 Nucleic Acids Res. 23, 277-284, 1995  
 A:Title: High affinity binding sites for the Wt1ms' tumour suppressor protein Wt1.  
 A:Reference number: I58315; MUID:95166449  
 A:Accession: I58315  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 'MGHHNNHHNHHSGHTEGRM',301-364,'F',366-386,'T',388-407,411-449 <HAM>  
 A:Cross-references: GB:S75264; NID:q986246; PID:AAA33443.1; PID:q896247  
 A:Note: this sequence is engineered  
 C:Genetics:  
 A:Gene: GDB:WT1  
 A:Cross-references: GDB:120496; OMIM:194070  
 A:Map position: 11p13-11p13  
 A:Insertions: 148/1; 223/2; 249/2; 266/2; 298/3; 349/1; 379/1; 410/1  
 A:Note: mRNA transcripts containing both alternatively spliced regions are the most abun  
 C:Keywords: alternative splicing; DNA binding; kidney; tumor suppressor; zinc finger  
 F:1-449/Product: Wt1ms tumor susceptibility protein Wt1, splice form 1 #status predicted  
 F:1-407,411-449/Product: Wt1ms tumor susceptibility protein Wt1, splice form 4 #status F  
 F:1-249,267-449/Product: Wt1ms tumor susceptibility protein Wt1, splice form 3 #status F  
 F:1-249,267-407,411-449/Product: Wt1ms tumor susceptibility protein Wt1, splice form 2 #

Query Match 100.0%; Score 123; DB 2; Length 449;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-11;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMPNAPYLSCL 23  
 DB 117 PSQASSGQARMPNAPYLSCL 139

RESULT 3  
 A39692  
 Wt1ms' tumor protein analog, Wt1 - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 16-Feb-1997  
 C:Accession: A39692  
 R:Buckler, A.J.; Pelletier, J.; Haber, D.A.; Glaser, T.; Housman, D.E.

Mol. Cell. Biol. 11, 1707-1712, 1991  
 A:Title: Isolation, characterization, and expression of the murine Wt1ms' tumor gene  
 A:Reference number: A39692; MUID:91141522  
 A:Accession: A39692  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-449 <BUC>  
 A:Cross-references: GB:M55512  
 C:Keywords: alternative splicing; DNA binding; transcription regulation; tumor suppre

Query Match 100.0%; Score 123; DB 2; Length 449;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-11;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMPNAPYLSCL 23  
 DB 117 PSQASSGQARMPNAPYLSCL 139

RESULT 4  
 JCS046  
 Wt1ms' tumor suppressor protein - African clawed frog  
 N:Alternate names: Wt1  
 C:Species: Xenopus laevis (African clawed frog)  
 C:Date: 31-Jan-1997 #sequence\_revision 31-Jan-1997 #text\_change 31-Jan-1997  
 C:Accession: JCS046  
 R:Semba, K.; Saito-Ueno, R.; Takayama, G.; Kondo, M.  
 Gene 175, 167-172, 1996  
 A:Title: cDNA cloning and its pronephros-specific expression of the Wt1ms' tumor supp  
 A:Reference number: JCS046; MUID:9707467  
 A:Accession: JCS046  
 A:Contents: testis  
 A:Molecule type: mRNA  
 A:Residues: 1-410 <SEM>  
 A:Cross-references: DBJ:DB2051  
 C:Comment: This protein is involved in kidney morphogenesis.  
 C:Genetics:  
 A:Gene: wcl

Query Match 83.7%; Score 103; DB 2; Length 410;  
 Best Local Similarity 78.3%; Pred. No. 2.7e-08;  
 Matches 18; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSQASSGQARMPNAPYLSCL 23  
 DB 98 PSQATTGQARMPNAPYLSCL 120

RESULT 5  
 S02660  
 9K protein (clone pg4) - human  
 C:Species: Homo sapiens (man)  
 C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 21-Jul-2000  
 C:Accession: S02660  
 R:Ramers, R.; Gross, G.; Mayr, U.; Collins, J.  
 Eur. J. Biochem. 178, 93-99, 1988  
 A:Title: Alternative mechanisms for gene activation induced by poly(ri) \* poly(rC) an  
 A:Reference number: S02660; MUID:89078418  
 A:Accession: S02660  
 A:Molecule type: mRNA  
 A:Residues: 1-82 <LAM>  
 A:Cross-references: EMBL:X13956; NID:q32574; PID:CAA32138.1; PID:q32575

Query Match 42.3%; Score 52; DB 2; Length 82;  
 Best Local Similarity 47.8%; Pred. No. 0.38;  
 Matches 11; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 PSQASSGQARMPNAPYLSCL 23  
 DB 23 PLEASSTRARVPCPLPYADCP 45

RESULT 6  
E82999  
Probable beta-ketoacyl synthase PA5174 [imported] - *Pseudomonas aeruginosa* (strain PA01)  
C:Species: *Pseudomonas aeruginosa*  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 15-Sep-2000  
C:Accession: E82999  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapid, K.; Lim,  
.; Lory, S.; Olson, M.V.  
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho  
Nature 406, 955-964, 2000  
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho  
A:Reference number: A82950  
A:Accession: E82999  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-634 <STO>  
A:Cross-references: GB:AE004930; GB:AE004091; NID:g95j1472; PIDN:AG08559; L: GSPDB:GN001  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA5174

Query Match	39.8%	Score 49	DB 2	Length 634
Best Local Similarity	47.8%	Pred. No. 9.5		
Matches 11	Conservative	3	Mismatches	4
			Indels	1
			Gaps	
OY	5	SSCOARMF----	PNAPYLSQLE	23
Db	296	ISGOARVIVGNSFAPIPECIE		318

```

RESULT      7
S61189
probable membrane protein YDR303c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein D9740.13
C:Species: Saccharomyces cerevisiae
C:Date: 23-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 29-Oct-1999
C:Accession: S61189
R: Ding, H.
submitted to the EMBL Data Library, June 1995
A:Description: The sequence of S. cerevisiae cosmid 9740.
A:Reference number: S61159
A:Accession: S61189
A:Molecule type: DNA
A:Residues: 1-885 <DIN>
A:Cross-references: EMBL:U28374; NID:9849207; PIDDN:RAB64739.1; PID:9849220; GSPDB:GN000000000
C:Genetics:
A:Gene: MIP5:YDR303c
A:Map position: 4R
C:Superfamily: unassigned GAL4-type zinc cluster proteins; GAL4 zinc binuclear cluster
C:Keywords: transmembrane protein
E:9-4/Domain: GAL4 zinc binuclear cluster homology <GALA>
E:422-438/Domain: transmembrane #status predicted <TM1>
E:699-715/Domain: transmembrane #status predicted <TM2>

```

Query Match	39.8%	Score 49;	DB 2;	Length 885;
Best Local Similarity	50.0%	Pred. No. 14;		
Matches 10; Conservative		1; Mismatches	9; Indels	0; Gaps 0;

```

      .qy      1 PSQASSGQARMFPNAPYLPS 20
                ||:||| | ||| |
Db            53 PSSSSSSNTQQVANGPYLNS 72

```

```

RESULT      8
179500      myc protein - human
             C:Species: Homo sapiens (man)
             C:date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 05-Nov-1999
             C:Accession: I79500

```

R:Fluwer, S.N., Nishikura, K.; Finger, L.R.; Halatska, F.G.; Eflman, J.; Nowell, P.C.;  
Proc. Natl. Acad. Sci. U.S.A. 85, 3052-3056, 1988  
A:Title: Sequence analysis of the MYC oncogene involved in the t(8;14)(q24,q11) chrom  
A:Reference number: 159116; MUID:88203638  
A:Accession: 179500  
A:Status: preliminary; translated from GR/EMBL/DDaj  
A:Molecule type: DNA  
A:Residues: 1188 <RS>  
A:Cross-references: GB:J02253; MID:q188976; PIDM:AA59887.1; PID:q188977

Query Match	39.0%;	Score 48;	DB 2;	Length 188;
Best Local Similarity	72.7%;	Pred. No. 3.8;		
Matches	8;	Conservative	1;	Mismatches 2;
				Indels 0;
				Gaps 0;

```
QY      13 PNAFYLPSCLE 23
          | | : | | | | |
Db      22 PGRPWLPSCLE 32
```

RESULT 9

JU0451

hypothetical 21k protein (c-myc 5' region) - chimpanzee

C:Species: Pan troglodytes (chimpanzee)

C:Date: 30-Sep-1991 #sequence-revision 30-Sep-1991 #text-change 21-Jul-2000

C:Accession: JU0451

R:Arnaud, C.; Rigole, M.; Eldard, M.E.; Galibert, F.

Gene 97, 231-237, 1991

A>Title: Cloning and nucleotide sequence of the chimpanzee c-myc gene.

A:Reference number: JU0449; MIMD:91153652

A:Accession: JU0451

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-188 <AAG>

A:Cross-references: GB:M38057; NID:g176652; PIDN:AA72909.L; PID:g176655

Query Match	39.0%;	Score 48;	DB 2;	Length 188;
Best Local Similarity	72.7%;	Pred. No. 3.8;		
Matches	8;	Conservative	1;	Mismatches 2; Indels 0; Gaps 0.

QY	13	PNAPYLPSCLE	23
		:	
Db	22	PGRPWLPSCLE	32

```

RESULT 10
I59116
myc protein - human
C:Species: Homo sapiens (man)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 05-Nov-1999
C:Accession: I59116
R:Flyover, S.N.; Nishikura, K.; Finger, L.R.; Haluska, F.G.; Finan, J.; Nowell, P.C.;
Proc. Natl. Acad. Sci. U.S.A. 85, 3052-3056, 1988
A:Title: Sequence analysis of the MYC oncogene involved in the t(8;14)(q24;q11) chrom
A:Reference number: I59116; MUID:88203638
A:Accession: I59116
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-168 <RES>
A:Cross-references: GB: M20605; NID: g188974; PIDN: AAA59886.1; PID: g188975

```

Query Match	39.0%	Score 48;	DB 2;	Length 188;
Best Local Similarity	72.7%	Pred. No. 3, 8;		
Matches	8;	Mismatches	2;	Gaps 0;

```

QY      13 PNAPYLPSCLE 23
        | | : | | | | |
Db      22 PGRPWLPSCLE 32

```

## RESULT 11

A29867  
hypothetical 20K protein (myc 5' region) (Burkitt lymphoma) - human  
C.Species: Homo sapiens (man)  
C.Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 18-Jun-1993  
C.Accession: A29867  
R.Showe, L.C.; Moore, R.C.A.; Erikson, J.; Croce, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 84, 2824-2828, 1987  
A.Title: MYC oncogene involved in a t(8;22) chromosome translocation is not altered in  
A.Reference number: A29867; MUID:87204220  
A.Accession: A29867  
A.Molecule type: DNA  
A.Residues: 14168 <SHO>

Query Match	39.0%	Score 48:	DB 2:	Length 188:
Best Local Similarity	72.7%	Pred. No. 3.8:		
Matches	8:	Conservative	1:	Mismatches 2: Indels 0: Gaps 0:
Oy	13	PNAAPLPSCLE	23	
		111111111		
Db	22	PERPWLPSCLE	32	

RESULT 12  
D83286  
hypothetical protein PA2886 [imported] - *Pseudomonas aeruginosa* (strain PA01)  
C:Species: *Pseudomonas aeruginosa*  
C:Date: 15-Sep-2000 #sequence-revision 15-Sep-2000 #text-change 15-Sep-2000  
C:Accession: D83286  
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardly, K.; Lim,  
J.; Lory, S.; Olson, M.V.  
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho  
gen.  
A:Reference number: A82950  
A:Accession: D83286  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-600 <STO>  
A:Cross-references: GB:AE004771; GB:AE004091; MID:G9948965; PIDN:AA606274.1; GSPDB:GN001  
A:Experimental source: strain PA01  
C:Genetics:  
C:Gene: PA2886

Query Match	39.0%	Score 48;	DB 2;	Length 600;
Best Local Similarity	47.4%	Pred. No. 13;		
Matches	9;	Conservative 3;	Mismatches 7;	Indels 0;
Gaps	0;			
QY	4	ASSGQARMPNAPFLPSC	22	
Db	125	AKSGIRENFSDAEPMPCV	143	

RESULT 13  
S68450  
apoptosis inhibitor hiap-2 - human  
C:Species: Homo sapiens (man)  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_Change 21-Jul-2000  
C:Accession: S68450  
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Chertton-Horvat, G.; Farahani  
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP  
A:Reference number: A58182; MUID:96149249  
A:Accession: S68450  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-618 <LIS>  
A:Cross-references: EMBL:U05879; NID:g1184317; PIDN:AAC5072.1; PID:g1184318  
C:Function:  
A:Description: apoptotic suppressor  
C:Superfamily: RING finger homology  
C:Keywords: apoptosis; zinc finger

F;567-611/Domain: RING finger homology &lt;RING&gt;

```

Query Match          39.0%; Score 48; DB 2; Length 618;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Oy 4 ASSQARPPNAPYLSCLE 23
    | | | | | | | | | |
Db 236 AMSEHRHFPNCPLENSLE 255

```

RESULT 14  
117679  
proline-rich protein A189r - Chlorella virus PBCV-1  
C:Species: Chlorella virus PBCV-1  
C:Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T17679  
R:Graves, M.V.; Van Etten, J.L.  
submitted to the EMBL Data Library, May 1999  
A:Reference number: Z18806  
A:Accession: T17679  
A:Status: preliminary: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-778 <GRA>  
A:Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAQ96557.1  
A:Experimental source: specific host Chlorella strain NC64A  
C:Genetics:  
A:Note: A189R

Query Match	39.0%	Score 48	DB 2	Length 778
Best Local Similarity	47.1%	Pred NO. 17		
Matches	8	Conservative	4	Mismatches 5
				Indels 0
				Gaps 0
QY	1	PSQSSGQARMPENAPY	17	
		: :   :   :   :		
Db	170	PKQSSGSGAGLKNRPF	186	

RESULT 15  
 JC4584  
 Insulin-like growth factor binding protein-5 precursor - pig  
 C:Species: Sus scrofa domestica (domestic pig)  
 C:Date: 10-Apr-1996 #sequence\_revision 24-May-1996 #text\_change 05-Nov-1999  
 C:Accession: J04584; G23734  
 R:White, M.E.; Diao, R.; Hathaway, M.R.; Mickelson, J.; Dayton, W.R.  
 Biochem. Biophys. Res. Commun. 218, 248-253, 1996  
 A>Title: Molecular cloning and sequence analysis of the porcine insulin-like growth f  
 A:Reference number: J04584; MUID:96136309  
 A:Accession: J04584  
 A:Molecule type: mRNA  
 A:Residues: 1-271 <WHI>  
 A:Cross-references: GB:041340; NID:q1173906; PIDN:AAA87859.1; PID:q1173907  
 A:Experimental source: skeletal muscle  
 R:Shimasaki, S.; Gao, L.; Shimonaka, M.; Ling, N.  
 Mol. Endocrinol. 5, 938-948, 1991  
 A>Title: Isolation and molecular cloning of insulin-like growth factor-binding protei  
 A:Reference number: A23734; MUID:92049376  
 A:Accession: G23734  
 A:Molecule type: protein  
 A:Residues: 20-25 'X', 27-28, 'X', 30-36, 'X', 38-39 <SHI>  
 C:Comment: This protein has essential roles in the regulation and coordination of ins  
 lays a role during myoblast proliferation and differentiation, and is important in th  
 C:Superfamily: Insulin-like growth factor binding protein 1; thyroglobulin type I rep  
 C:Keywords: differentiation; growth factor; skeletal muscle  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-271/Product: insulin-like growth factor binding protein-5 #status experimental <  
 F:131-262/Domain: thyroglobulin type I repeat homology <THYI>

Query Match	38.28;	Score 47;	DB 2;	Length 271;
Best Local Similarity	47.48;	Pred. No. 8;		

Matches	9;	Conservative	1;	Mismatches	9;	Indels	0;	Gaps	0;
Qy	3	QASSGQARMFPNAPYLPSG	21						
Db	200	QELKASPRMVPRAVYLLPNC	218						

Search completed: April 11, 2001, 14:02:32  
 Job time: 527 sec

1. The first part of the paper is devoted to a general discussion of the problem of the existence of solutions of the system of equations (1) for arbitrary values of the parameters  $\alpha$  and  $\beta$ . It is shown that the system has solutions for all values of the parameters  $\alpha$  and  $\beta$  if the function  $f(x)$  is continuous and has a bounded derivative.

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OM protein - protein search, using sw model

Run on: April 11, 2001, 13:54:44 ; Search time 42.4 Seconds  
(without alignments)  
89.423 Million cell updates/sec

Title: US-09-164-223-2

Perfect score: 123  
1 PSQASSGQARMFPNAPYLPSCLE 23

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1027871 seqs, 16484993 residues

Total number of hits satisfying chosen parameters: 1027871

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Pending Patents-AA:\*  
1: /cgn2\_6/ptodata/2/paa/US086\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/paa/US07\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/paa/US080\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/paa/US081\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/paa/US082\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/paa/US083\_COMB.pep:\*  
7: /cgn2\_6/ptodata/2/paa/US084\_COMB.pep:\*  
8: /cgn2\_6/ptodata/2/paa/US085\_COMB.pep:\*  
9: /cgn2\_6/ptodata/2/paa/US086\_COMB.pep:\*  
10: /cgn2\_6/ptodata/2/paa/US087\_COMB.pep:\*  
11: /cgn2\_6/ptodata/2/paa/US088\_COMB.pep:\*  
12: /cgn2\_6/ptodata/2/paa/US089\_COMB.pep:\*  
13: /cgn2\_6/ptodata/2/paa/US090\_COMB.pep:\*  
14: /cgn2\_6/ptodata/2/paa/US091\_COMB.pep:\*  
15: /cgn2\_6/ptodata/2/paa/US092\_COMB.pep:\*  
16: /cgn2\_6/ptodata/2/paa/US093\_COMB.pep:\*  
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18: /cgn2\_6/ptodata/2/paa/US095\_COMB.pep:\*  
19: /cgn2\_6/ptodata/2/paa/US096\_COMB.pep:\*  
20: /cgn2\_6/ptodata/2/paa/US097\_COMB.pep:\*  
21: /cgn2\_6/ptodata/2/paa/US098\_COMB.pep:\*  
22: /cgn2\_6/ptodata/2/paa/US099\_COMB.pep:\*  
23: /cgn2\_6/ptodata/2/paa/US100\_COMB.pep:\*  
24: /cgn2\_6/ptodata/2/paa/US101\_COMB.pep:\*  
25: /cgn2\_6/ptodata/2/paa/US102\_COMB.pep:\*  
26: /cgn2\_6/ptodata/2/paa/US103\_COMB.pep:\*  
27: /cgn2\_6/ptodata/2/paa/US104\_COMB.pep:\*  
28: /cgn2\_6/ptodata/2/paa/US105\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	123	100.0	23	US-09-164-223-2	Sequence 2, Appli
2	123	100.0	23	US-09-164-223-3	Sequence 3, Appli
3	123	100.0	23	US-09-164-223-2	Sequence 2, Appli
4	123	100.0	23	US-09-164-223-2	Sequence 3, Appli
5	123	100.0	23	US-09-164-223-2	Sequence 2, Appli

6	123	100.0	23	US-09-164-223-3	Sequence 3, Appli
7	123	100.0	23	US-09-276-484-2	Sequence 2, Appli
8	123	100.0	23	US-09-276-484-3	Sequence 2, Appli
9	123	100.0	23	US-09-276-484A-2	Sequence 2, Appli
10	123	100.0	23	US-09-276-484A-3	Sequence 2, Appli
11	123	100.0	23	US-09-523-419-2	Sequence 2, Appli
12	123	100.0	23	US-09-523-419-3	Sequence 2, Appli
13	123	100.0	23	US-09-679-339-2	Sequence 2, Appli
14	123	100.0	23	US-09-679-339-3	Sequence 2, Appli
15	123	100.0	23	US-09-684-361-2	Sequence 2, Appli
16	123	100.0	23	US-09-684-361-3	Sequence 2, Appli
17	123	100.0	23	US-09-685-830-2	Sequence 2, Appli
18	123	100.0	23	US-09-685-830-3	Sequence 2, Appli
19	123	100.0	23	US-09-785-019-2	Sequence 2, Appli
20	123	100.0	23	US-09-785-019-3	Sequence 2, Appli
21	123	100.0	23	US-09-791-477-2	Sequence 2, Appli
22	123	100.0	23	US-09-791-477-3	Sequence 2, Appli
23	123	100.0	152	US-09-785-019-343	Sequence 343, App
24	123	100.0	154	US-09-037-179A-5	Sequence 5, Appli
25	123	100.0	154	US-09-037-179A-6	Sequence 5, Appli
26	123	100.0	256	US-09-785-019-335	Sequence 335, App
27	123	100.0	345	US-09-037-179A-2	Sequence 2, Appli
28	123	100.0	345	US-09-037-179A-3	Sequence 3, Appli
29	123	100.0	369	US-09-785-019-346	Sequence 346, App
30	123	100.0	410	US-09-785-019-333	Sequence 333, App
31	123	100.0	449	US-09-037-179A-4	Sequence 4, Appli
32	123	100.0	449	US-09-037-179A-5	Sequence 5, Appli
33	123	100.0	449	US-09-164-223-319	Sequence 319, App
34	123	100.0	449	US-09-164-223-320	Sequence 320, App
35	123	100.0	449	US-09-164-223-319	Sequence 319, App
36	123	100.0	449	US-09-164-223-319	Sequence 319, App
37	123	100.0	449	US-09-164-223-319	Sequence 319, App
38	123	100.0	449	US-09-164-223-319	Sequence 319, App
39	123	100.0	449	US-09-276-484-319	Sequence 319, App
40	123	100.0	449	US-09-276-484-320	Sequence 320, App
41	123	100.0	449	US-09-276-484A-319	Sequence 319, App
42	123	100.0	449	US-09-276-484A-320	Sequence 320, App
43	123	100.0	449	US-09-523-419-319	Sequence 319, App
44	123	100.0	449	US-09-523-419-320	Sequence 320, App
45	123	100.0	449	US-09-791-477-320	Sequence 320, App

## ALIGNMENTS

RESULT 1  
US-09-164-223-2  
Sequence 2, Application US/09164223  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: Cheever, Martin A.  
TITLE OR INVENTION: COMPOSITIONS AND METHODS FOR WT1 SPECIFIC IMMUNOTHERAPY  
FILE REFERENCE: 210121.465  
CURRENT APPLICATION NUMBER: US/09/164,223  
CURRENT FILING DATE: 1998-09-30  
NUMBER OF SEQ ID NOS: 320  
SOFTWARE: Patentlin Ver. 2.0  
SEQ ID NO 2  
LENGTH: 23  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-164-223-2

Query Match 100.0%; Score 123; DB 15; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3.6e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PSQASSGQARMFPNAPYLPSCLE 23  
DB 1 PSQASSGQARMFPNAPYLPSCLE 23

```

RESULT 2
US-09-164-223-3
: Sequence 3, Application US/09164223
: GENERAL INFORMATION:
: APPLICANT: Gaiger, Alexander
: APPLICANT: Cheever, Martin A.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1 SPECIFIC IMMUNOTHERAPY
: FILE REFERENCE: 210121.465
: CURRENT APPLICATION NUMBER: US/09/164,223
: CURRENT FILING DATE: 1998-09-30
: NUMBER OF SEQ ID NOS: 320
: SOFTWARE: PatentIn ver. 2.0
: SEQ ID NO 3
: LENGTH: 23
: TYPE: PRT
: ORGANISM: Mus musculus
US-09-164-223-3

```

Query Match	100.0%;	Score 123;	DB 15;	Length 23;
Best Local Similarity	100.0%;	Pred. No. 3.6e-11;		
Matches	23;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;
QY	1	PSQASSQQAAMFPNAPLPSCLE	23	
Db	1	PSQASSQQAAMFPNAPLPSCLE	23	

```

RESULT 3
US-09-164-223-2
: Sequence 2, Application US/09164223A
: GENERAL INFORMATION:
: APPLICANT: Gaiger, Alexander
: APPLICANT: Cheever, Martin A.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1 SPECIFIC IMMUNOTHERAPY
: FILE REFERENCE: 210121.465
: CURRENT APPLICATION NUMBER: US/09/164,223A
: CURRENT FILING DATE: 1998-09-30
: NUMBER OF SEQ ID NOS: 320
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 23
: TYPE: PRF
: ORGANISM: Homo sapiens
: US-09-164-223-2

```

	Query Match	100.0%	Score 123;	DB 15;	Length 23;
	Best Local Similarity	100.0%;	Pred. NO.3.6e-11;		
	Matches 23; Conservative	0;	Mismatches	0;	Gaps
QY	1 PSQAASSGAARMPNAPFLPSCLE	23			
Db	1 PSQAASSGAARMPNAPFLPSCLE	23			

```

RESULT      4
US-09-164-223-3
: Sequence 3, Application US/09164223A
: GENERAL INFORMATION:
: APPLICANT: Gaiger, Alexander
: APPLICANT: Cheever, Martin A.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTL SPECIFIC IMMUNOTHERAPY
: FILE REFERENCE: 210121.465
: CURRENT APPLICATION NUMBER: US/09/164,223A
: CURRENT FILING DATE: 1998-09-30
: NUMBER OF SEQ ID NOS: 320
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 3
: LENGTH: 23
: TYPE: PRT
: ORGANISM: Mus musculus
: US-09-164-223-3

```

Query March	100.0%;	Score 123;	DB 15;
Best Local Similarity	100.0%;	Pred. No. 3	6e-11;
Matches 23; Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;

```

RESULT      5
US-09-164-223-2
: Sequence 2 Application US/09164223B
: GENERAL INFORMATION:
: APPLICANT: Galger, Alexander
: APPLICANT: Cheever, Martin A.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI SPECIFIC IMMUNOTHERAPY
: FILE REFERENCE: 210121.465
: CURRENT APPLICATION NUMBER: US/09/164,223B
: CURRENT FILING DATE: 1998-09-30
: NUMBER OF SEQ ID NOS: 320
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 23
: TYPE: prt
: ORGANISM: Homo sapiens
: US-09-164-223-2

```

Query Match	100.0%;	Score 123;	DB 15;	Length 23;
Best Local Similarity	100.0%;	Pred. No. 3	6e-11;	
Matches 23;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	PSQASSGQARMPNAPILPSCLE	23	
Db	1	PSQASSGQARMPNAPILPSCLE	23	

```

RESULT      6
US-09-164-223-3
: Sequence 3. Application US/09164223B
: GENERAL INFORMATION:
: APPLICANT: Galger, Alexander
: APPLICANT: Cheever, Martin A.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI SPECIFIC IMMUNOTHERAPY
: FILE REFERENCE: 210121.465
: CURRENT APPLICATION NUMBER: US/09/164.223B
: CURRENT FILING DATE: 1998-09-30
: NUMBER OF SEQ ID NOS: 320
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 3
: LENGTH: 23
: TYPE: prt
: ORGANISM: Mus musculus
: US-09-164-223-3

```

Query Match	100.0%	Score 123;	DB 15;	Length 23;
Best Local Similarity	100.0%	Pred. NO.3.6e-11;		
Matches 23;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	PSQASSGQARMPNAPYPSCLE	23	
Db	1	PSQASSGQARMPNAPYPSCLE	23	

RESULT 7  
US-09-276-484-2  
; Sequence 2, Application US/09276484  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Cheever, Martin A.



TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
FILE OF INVENTION: SPECIFIC IMMUNOTHERAPY  
FILE REFERENCE: 210121.465C1  
CURRENT APPLICATION NUMBER: US/09/276,484  
CURRENT FILING DATE: 1999-03-25  
NUMBER OF SEQ ID NOS: 326  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 23  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-276-484-2

Query Match 100.0%; Score 123; DB 16; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3.6e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMFPNAPYLPSCLE 23  
Db 1 PSQASSGQARMFPNAPYLPSCLE 23

RESULT 8  
US-09-276-484-3  
Sequence 3, Application US/09276484  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: Cheever, Martin A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
FILE REFERENCE: 210121.465C1  
CURRENT APPLICATION NUMBER: US/09/276,484  
CURRENT FILING DATE: 1999-03-25  
NUMBER OF SEQ ID NOS: 326  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 3  
LENGTH: 23  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-276-484-3

Query Match 100.0%; Score 123; DB 16; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3.6e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMFPNAPYLPSCLE 23  
Db 1 PSQASSGQARMFPNAPYLPSCLE 23

RESULT 9  
US-09-276-484A-2  
Sequence 2, Application US/09276484A  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: Cheever, Martin A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1 SPECIFIC  
FILE REFERENCE: 210121.465C1  
CURRENT APPLICATION NUMBER: US/09/276,484A  
CURRENT FILING DATE: 1999-03-25  
PRIOR APPLICATION NUMBER: US 09/164,223  
PRIOR FILING DATE: 1999-09-30  
NUMBER OF SEQ ID NOS: 326  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 23  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-276-484A-2

Query Match 100.0%; Score 123; DB 16; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3.6e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMFPNAPYLPSCLE 23  
Db 1 PSQASSGQARMFPNAPYLPSCLE 23

RESULT 10  
US-09-276-484A-3  
Sequence 3, Application US/09276484A  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: Cheever, Martin A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1 SPECIFIC  
FILE REFERENCE: 210121.465C1  
CURRENT APPLICATION NUMBER: US/09/276,484A  
CURRENT FILING DATE: 1999-03-25  
PRIOR APPLICATION NUMBER: US 09/164,223  
PRIOR FILING DATE: 1999-09-30  
NUMBER OF SEQ ID NOS: 326  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 23  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-276-484A-3

Query Match 100.0%; Score 123; DB 16; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3.6e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMFPNAPYLPSCLE 23  
Db 1 PSQASSGQARMFPNAPYLPSCLE 23

RESULT 11  
US-09-523-419-2  
Sequence 2, Application US/09523419  
GENERAL INFORMATION:  
APPLICANT: Hendrickson, Ronald C.  
APPLICANT: Probst, Peter  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND THERAPY  
FILE REFERENCE: 210121.492  
CURRENT APPLICATION NUMBER: US/09/523,419  
CURRENT FILING DATE: 2000-03-10  
NUMBER OF SEQ ID NOS: 326  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 23  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-523-419-2

Query Match 100.0%; Score 123; DB 19; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3.6e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMFPNAPYLPSCLE 23  
Db 1 PSQASSGQARMFPNAPYLPSCLE 23

RESULT 12  
US-09-523-419-3

```

; Sequence 3, Application US/09523419
; GENERAL INFORMATION:
; APPLICANT: Hendrickson, Ronald C.
; APPLICANT: Probst, Peter
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND THERAPY
; FILE REFERENCE: 210121.492
; CURRENT APPLICATION NUMBER: US/09/523,419
; CURRENT FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-523-419-3

```

```

Query Match          100.0%; Score 123; DB 19; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 PSQASSGOARMPNAPYLPSCLE 23
Db 1 PSQASSGOARMPNAPYLPSCLE 23

```

```

RESULT 13
US-09-679-339-2
; Sequence 2, Application US/09679339
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Xu, Jiangchun
; APPLICANT: Cheever, Martin G.
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.533
; CURRENT APPLICATION NUMBER: US/09/679,339
; CURRENT FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-679-339-2

```

```

Query Match          100.0%; Score 123; DB 20; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 PSQASSGOARMPNAPYLPSCLE 23
Db 1 PSQASSGOARMPNAPYLPSCLE 23

```

```

RESULT 14
US-09-679-339-3
; Sequence 3, Application US/09679339
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Xu, Jiangchun
; APPLICANT: Cheever, Martin G.
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.533
; CURRENT APPLICATION NUMBER: US/09/679,339
; CURRENT FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 357

```

```

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-679-339-3

```

```

Query Match          100.0%; Score 123; DB 20; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 PSQASSGOARMPNAPYLPSCLE 23
Db 1 PSQASSGOARMPNAPYLPSCLE 23

```

```

RESULT 15
US-09-684-361-2
; Sequence 2, Application US/09684361
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C2
; CURRENT APPLICATION NUMBER: US/09/684,361
; CURRENT FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-684-361-2

```

```

Query Match          100.0%; Score 123; DB 20; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 PSQASSGOARMPNAPYLPSCLE 23
Db 1 PSQASSGOARMPNAPYLPSCLE 23

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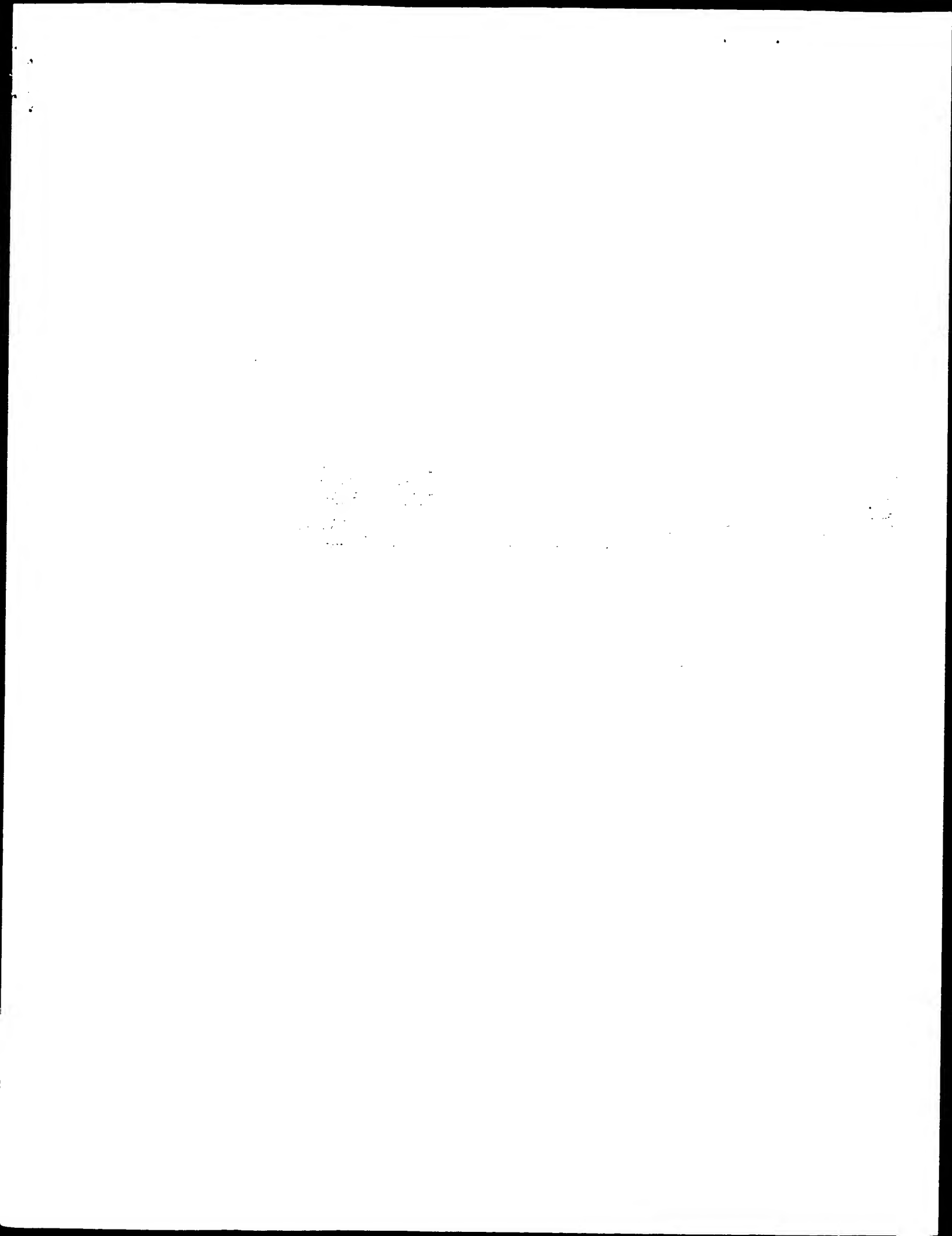
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Job time: 512 sec

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Fri Apr 20 12:06:13 2001

us-09-164-223-2.rap



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2001, 13:53:35 ; Search time 12.38 Seconds  
(without alignments)  
33.361 Million cell updates/sec

Title: US-09-164-223-2

Sequence: 1 PSQSSSQARMFPNAPLPSCLE 23

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: /cgn2\_6/prodata/2/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/2/1aa/5B\_COMB.pep:\*  
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4: /cgn2\_6/prodata/2/1aa/PCPUS\_COMB.pep:\*  
5: /cgn2\_6/prodata/2/1aa/backup1est1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	123	100.0	154	1 US-08-102-942A-5	Sequence 5, Appl1
2	123	100.0	210	1 US-08-234-783-2	Sequence 2, Appl1
3	123	100.0	210	1 US-08-456-907-2	Sequence 2, Appl1
4	123	100.0	210	4 PCT-US95-05523-2	Sequence 2, Appl1
5	123	100.0	345	1 US-08-102-942A-2	Sequence 2, Appl1
6	123	100.0	429	1 US-08-234-783-4	Sequence 4, Appl1
7	123	100.0	429	1 US-08-456-907-4	Sequence 4, Appl1
8	123	100.0	429	4 PCT-US95-05523-4	Sequence 4, Appl1
9	123	100.0	449	4 US-08-102-942A-4	Sequence 4, Appl1
10	123	100.0	449	1 US-08-102-942A-6	Sequence 6, Appl1
11	123	100.0	438	1 PCT-US95-05922A-2	Sequence 2, Appl1
12	48	39.0	618	2 US-08-511-485-8	Sequence 8, Appl1
13	48	39.0	618	3 US-09-212-971-8	Sequence 8, Appl1
14	48	39.0	618	3 US-08-800-929A-8	Sequence 8, Appl1
15	48	39.0	618	4 PCT-US96-12860-2	Sequence 2, Appl1
16	47	38.2	186	1 US-08-698-551-6	Sequence 6, Appl1
17	47	38.2	186	2 US-08-602-228-6	Sequence 6, Appl1
18	47	38.2	186	2 US-08-649-341A-6	Sequence 6, Appl1
19	47	38.2	186	2 US-08-494-440B-6	Sequence 6, Appl1
20	47	38.2	186	2 US-08-533-901B-6	Sequence 6, Appl1
21	47	38.2	186	2 US-08-839-032A-6	Sequence 6, Appl1
22	47	38.2	186	2 US-08-839-031A-6	Sequence 6, Appl1
23	47	38.2	186	4 PCT-US95-12724-6	Sequence 4, Appl1
24	47	38.2	271	4 PCT-US92-01196-3	Sequence 3, Appl1
25	47	38.2	272	1 US-08-698-551-8	Sequence 8, Appl1
26	47	38.2	272	2 US-08-602-228-8	Sequence 8, Appl1
27	47	38.2	272	2 US-08-649-341A-8	Sequence 8, Appl1
28	47	38.2	272	2 US-08-494-440B-8	Sequence 8, Appl1

29	47	38.2	272	2	US-08-533-901B-8	Sequence 8, Appl1
30	47	38.2	272	2	US-08-839-032A-8	Sequence 8, Appl1
31	47	38.2	272	2	US-08-839-031A-8	Sequence 8, Appl1
32	47	38.2	272	4	PCT-US92-01196-4	Sequence 4, Appl1
33	47	38.2	272	4	PCT-US95-12724-8	Sequence 4, Appl1
34	44	35.8	717	5	5262177-5	Patent No. 5262177
35	44	35.8	719	2	US-08-520-933-3	Sequence 3, Appl1
36	44	35.8	738	5	5262177-2	Patent No. 5262177
37	43.5	35.4	94	1	US-08-208-008C-14	Sequence 14, Appl1
38	43.5	35.4	174	5	5256643-2	Patent No. 5256643
39	43.5	35.4	187	5	5256643-2	Sequence 3, Appl1
40	43.5	35.4	188	1	US-07-749-001-3	Sequence 3, Appl1
41	43.5	35.4	188	1	US-07-749-001-5	Sequence 5, Appl1
42	43.5	35.4	188	1	US-08-154-198-3	Sequence 3, Appl1
43	43.5	35.4	188	1	US-08-154-198-5	Sequence 5, Appl1
44	43.5	35.4	188	1	US-08-463-335-3	Sequence 3, Appl1
45	43.5	35.4	188	1	US-08-463-335-5	Sequence 5, Appl1

## ALIGNMENTS

RESULT 1  
US-08-102-942A-5  
Sequence 5, Application US/08102942A  
Patent No. 5726288  
GENERAL INFORMATION:  
APPLICANT: Call, Katherine M.  
APPLICANT: Glaser, Thomas M.  
APPLICANT: Ito, Caryn Y.  
APPLICANT: Buckler, Alan J.  
APPLICANT: Pelletier, Jerry  
APPLICANT: Haber, Daniel A.  
APPLICANT: Rose, Elise A.  
APPLICANT: Housman, David E.  
APPLICANT: Bruening, Wendy  
APPLICANT: Darveau, Andre  
TITLE OF INVENTION: Localization and Characterization of the  
TITLE OF INVENTION: Wlms' Tumor Gene  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: U.S.  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/102,942A  
FILING DATE: 02-AUG-1993  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Grahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: MIT-5194A2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 154 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-102-942A-5

GENERAL INFORMATION:  
APPLICANT: Heiljdt, Meenhard  
APPLICANT: Morris, Jennifer  
APPLICANT: Rauscher III, Frank J.  
APPLICANT: Rodeck, Ulrich  
TITLE OF INVENTION: WT1 Monoclonal Antibodies and Methods of  
TITLE OF INVENTION: Use Therefor  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:

ADDRESS: Howson and Howson  
STREET: Spring House Corporate Cntr, PO Box 45  
CITY: Spring House  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19477

```

1 COMPUTER READABLE FORM:
2 MEDIUM TYPE: Floppy disk
3 COMPUTER: IBM PC compatible
4 OPERATING SYSTEM: PC-DOS/MS-DOS
5 SOFTWARE: Patentin Release #1.0, Version #1.25
6 CURRENT APPLICATION DATA:
7 APPLICATION NUMBER: US/08/374 783

```

FILED DATE: 435  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION: 435

NAME: BAK, Mary E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: WST48USA  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-540-9200  
TELEFAX: 215-540-5818  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS

US-08-234-783-2

```

Query Match      100.0%; Score 123; DB 1; Length 210;
Best Local Similarity 100.0%; Pred. No. 7.6e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

2y 1 PSQASSGQARMPNAPYLPSCLE 23  
 |||||  
 128 PSQASSGQARMPNAPYLPSCLE 150  
 db

RESULT 3  
IS-08-456-907-2

Sequence 2, Application US/08456907  
Patent No. 5633142  
GENERAL INFORMATION:  
APPLICANT: Harlyn Moorhead

INVENTOR: Healy, Meinard  
APPLICANT: Morris, Jennifer  
APPLICANT: Rauscher III, Frank J.  
APPLICANT: Rodeck, Ulrich  
TITLE OF INVENTION: W1 Monoclonal Antibodies and Methods of  
TITLE OF INVENTION: Use Therefor

NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howson and Howson  
STREET: Spring House Corporate Cntr, PO Box 457  
CITY: Spring House  
STATE: Pennsylvania  
COUNTRY: USA

```

; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; COMMENTS:
;

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```

1  SOFTWARE: PatentInRelease #1.0,
2  CURRENT APPLICATION DATA:
3  APPLICATION NUMBER: US/08/456,907
4  FILING DATE:
5  CLASSIFICATION: 435
6  PRIOR APPLICATION DATA:
7

```

APPLICATION NUMBER: US 08/234,763  
FILING DATE: 28-APR-1994  
ATTORNEY/AGENT INFORMATION:

NAME: Bak, Maity E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: WST48AUSP  
TELECOMMUNICATION INFORMATION:  
;

TELEPHONE: 215-540-9200  
TELEFAX: 215-540-5818  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;

```

MOLECULE TYPE: protein  
US-08-456-907-2

```
Query Match      100.0%; Score 123; DB 1; Length 210;
Best Local Similarity 100.0%; Pred. No. 7.6e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0
```

QY 1 PSQASSGQARMFPNAPYLPSCLE 23  
 |||||  
 Db 128 PSQASSGQARMFPNAPYLPSCLE 150

RESULT 4  
PCT-US95-05523-2

```

; sequence 2, Application PC/TUS9505523
;
; GENERAL INFORMATION:
;
; APPLICANT: The Wistar Institute of Anatomy and Biology
;
; TITLE OF INVENTION: WT1 Monoclonal Antibodies and
;

```

TITLE OF INVENTION: Methods of use Therefore  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:

ADDRESS: Howson and Howson  
STREET: Spring House Corporate Cntr, PO Box 457  
CITY: Spring House  
STATE: Pennsylvania

COUNTRY: USA  
ZIP: 19477  
COMPUTER READABLE FORM

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0 Version #1.25

```

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/055233  
 FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/234,783  
FILING DATE: 28-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: WST48BCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-540-9200  
TELEFAX: 215-540-5818  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 210 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-05523-2

Query Match 100.0%; Score 123; DB 4; Length 210;  
Best Local Similarity 100.0%; Pred. No. 7.6e-12;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PSQASSGQARMFPNAPYLPSCLE 23  
DB 128 PSQASSGQARMFPNAPYLPSCLE 150

RESULT 5  
US-08-102-942A-2  
Sequence 2, Application US/08102942A  
Patent No. 5726288

GENERAL INFORMATION:  
APPLICANT: Call, Katherine M.  
APPLICANT: Glaser, Thomas M.  
APPLICANT: Ito, Caryn Y.  
APPLICANT: Buckler, Alan J.  
APPLICANT: Pelletier, Jerry  
APPLICANT: Haber, Daniel A.  
APPLICANT: Rose, Elise A.  
APPLICANT: Housman, David E.  
APPLICANT: Bruening, Wendy  
APPLICANT: Darveau, Andre  
TITLE OF INVENTION: Localization and Characterization of the  
TITLE OF INVENTION: Wilms' Tumor Gene  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: U.S.  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/102,942A  
FILING DATE: 02-AUG-1993  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: MIT-5194A2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 345 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-102-942A-2

Query Match 100.0%; Score 123; DB 1; Length 345;  
Best Local Similarity 100.0%; Pred. No. 1.3e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PSQASSGQARMFPNAPYLPSCLE 23  
DB 33 PSQASSGQARMFPNAPYLPSCLE 55

RESULT 6  
US-08-234-783-4  
Sequence 4, Application US/08234783  
Patent No. 5622835

GENERAL INFORMATION:  
APPLICANT: Herlyn, Meenhard  
APPLICANT: Morris, Jennifer  
APPLICANT: Rauscher III, Frank J.  
APPLICANT: Rodeck, Ulrich  
TITLE OF INVENTION: WT1 Monoclonal Antibodies and Methods of  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howson and Howson  
STREET: Spring House Corporate Cntr, PO Box 457  
CITY: Spring House  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19477

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/234,783  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Bak, Mary E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: WST48USA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-540-9200  
TELEFAX: 215-540-5818  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 429 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-234-783-4

Query Match 100.0%; Score 123; DB 1; Length 429;  
Best Local Similarity 100.0%; Pred. No. 1.7e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PSQASSGQARMFPNAPYLPSCLE 23  
DB 117 PSQASSGQARMFPNAPYLPSCLE 139

RESULT 7  
US-08-456-907-4  
Sequence 4, Application US/08456907  
Patent No. 5633142

GENERAL INFORMATION:  
APPLICANT: Herlyn, Meenhard  
APPLICANT: Morris, Jennifer  
APPLICANT: Rauscher III, Frank J.  
APPLICANT: Rodeck, Ulrich  
TITLE OF INVENTION: WT1 Monoclonal Antibodies and Methods of

;; TITLE OF INVENTION: Use Therefor  
;; NUMBER OF SEQUENCES: 7  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Howson and Howson  
;; STREET: Spring House Corporate Cntr, PO Box 457  
;; CITY: Spring House  
;; STATE: Pennsylvania  
;; COUNTRY: USA  
;; ZIP: 19477  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/456,907  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/234,783  
;; FILING DATE: 28-APR-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Bak, Mary E.  
;; REGISTRATION NUMBER: 31,215  
;; REFERENCE/DOCKET NUMBER: WST48AUSA  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 215-540-9200  
;; TELEFAX: 215-540-5818  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 429 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-456-907-4

Query Match 100.0%; Score 123; DB 1; Length 429;  
Best Local Similarity 100.0%; Pred. No. 1.7e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMFPNAPLPSCLE 23  
Db 117 PSQASSGQARMFPNAPLPSCLE 139

RESULT 8  
PCT-US95-05523-4  
;; Sequence 4, Application PC/TUS9505523  
;; GENERAL INFORMATION:  
;; APPLICANT: The Wistar Institute of Anatomy and Biology  
;; TITLE OF INVENTION: WTI Monoclonal Antibodies and  
;; NUMBER OF SEQUENCES: 7  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Howson and Howson  
;; STREET: Spring House Corporate Cntr, PO Box 457  
;; CITY: Spring House  
;; STATE: Pennsylvania  
;; COUNTRY: USA  
;; ZIP: 19477  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US95/05523  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/234,783  
;; FILING DATE: 28-APR-1994

;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Bak, Mary E.  
;; REGISTRATION NUMBER: 31,215  
;; REFERENCE/DOCKET NUMBER: WST48PCT  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 215-540-9200  
;; TELEFAX: 215-540-5818  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 429 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; PCT-US95-05523-4

Query Match 100.0%; Score 123; DB 4; Length 429;  
Best Local Similarity 100.0%; Pred. No. 1.7e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMFPNAPLPSCLE 23  
Db 117 PSQASSGQARMFPNAPLPSCLE 139

RESULT 9  
US-08-102-942A-4  
;; Sequence 4, Application US/08102942A  
;; Patent No. 5726288  
;; GENERAL INFORMATION:  
;; APPLICANT: Call, Katherine M.  
;; APPLICANT: Glaser, Thomas M.  
;; APPLICANT: Ito, Caryn Y.  
;; APPLICANT: Buckler, Alan J.  
;; APPLICANT: Pelletier, Jerry  
;; APPLICANT: Haber, Daniel A.  
;; APPLICANT: Rose, Elise A.  
;; APPLICANT: Housman, David E.  
;; APPLICANT: Bruening, Wendy  
;; APPLICANT: Darveau, Andre  
;; TITLE OF INVENTION: Localization and Characterization of the  
;; NUMBER OF SEQUENCES: 8  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
;; STREET: Two Millitia Drive  
;; CITY: Lexington  
;; STATE: Massachusetts  
;; COUNTRY: U.S.  
;; ZIP: 02173  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/102,942A  
;; FILING DATE: 02-AUG-1993  
;; CLASSIFICATION: 530  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Granahan, Patricia  
;; REGISTRATION NUMBER: 32,227  
;; REFERENCE/DOCKET NUMBER: MIT-5194A2  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 617-861-6240  
;; TELEFAX: 617-861-9540  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 449 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-102-942A-4



Query Match 100.0%; Score 123; DB 1; Length 449;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-11;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMPNAPYLPSCLE 23  
 |||  
 DB 117 PSQASSGQARMPNAPYLPSCLE 139

RESULT 10  
 US-08-102-942A-6

; Sequence 6, Application US/08102942A  
 ; Patent No. 5726288

GENERAL INFORMATION:

APPLICANT: Call, Katherine M.

APPLICANT: Glaser, Thomas M.

APPLICANT: Ito, Caryn Y.

APPLICANT: Buckler, Alan J.

APPLICANT: Pelletier, Jerry

APPLICANT: Haber, Daniel A.

APPLICANT: Rose, Elise A.

APPLICANT: Housman, David E.

APPLICANT: Darveau, Andre

APPLICANT: Brueening, Wendy

TITLE OF INVENTION: Localization and Characterization of the

TITLE OF INVENTION: Wilms' Tumor Gene

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: Massachusetts

COUNTRY: U.S.

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/102,942A

FILING DATE: 02-AUG-1993

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: MIT-5194A2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-861-6240

TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 449 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-102-942A-6

Query Match 100.0%; Score 123; DB 1; Length 449;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-11;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMPNAPYLPSCLE 23  
 |||  
 DB 117 PSQASSGQARMPNAPYLPSCLE 139

RESULT 11  
 PCT-US95-05922A-2

; Sequence 2, Application PC/TUS9505922A  
 ; GENERAL INFORMATION:

APPLICANT: HE, ET AL.

TITLE OF INVENTION: Human Inhibitor of Apoptosis Gene 1

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

ADDRESSEE: CECCHI, STEWART & OLSTEIN

STREET: 6 BECKER FARM ROAD

CITY: ROSELAND

STATE: NEW JERSEY

COUNTRY: USA

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/05922A

FILING DATE: 11 MAY 1995

CLASSIFICATION:

PRIOR APPLICATION NUMBER:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: FERRARO, GREGORY D.

REGISTRATION NUMBER: 36,134

REFERENCE/DOCKET NUMBER: 325800-292

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 438 AMINO ACIDS

TYPE: AMINO ACID

STRANDEDNESS:

TOPOLOGY: LINEAR

MOLECULE TYPE: PROTEIN

PCT-US95-05922A-2

Query Match 39.0%; Score 48; DB 4; Length 438;  
 Best Local Similarity 50.0%; Pred. No. 7.1;  
 Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 4 ASSGQARMPNAPYLPSCLE 23  
 |||  
 DB 56 AMSEHRRHFPNCPLENSLE 75

RESULT 12

US-08-511-485-8

; Sequence 8, Application US/08511485

; Patent No. 5919912

GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G.

APPLICANT: Mackenzie, Alexander E.

TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,

TITLE OF INVENTION: PROBES, AND DETECTION METHODS

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/511,485  
 FILING DATE: 04-AUG-1995  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Clark, Paul T.  
 REGISTRATION NUMBER: 30,162  
 REFERENCE/DOCKET NUMBER: 07540/002001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617/542-5070  
 TELEFAX: 617/542-8906  
 TELEX: 200154  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 618 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: both  
 MOLECULE TYPE: protein  
 US-08-511-485-8

Query Match 39.0%; Score 48; DB 2; Length 618;  
 Best Local Similarity 50.0%; Pred. No. 10;  
 Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 4 ASSGQARFNPAPYLPSCLE 23  
 DB 236 AMSEHRRHFPNCPLFENSL 255

RESULT 13  
 US-09-212-971-8  
 Sequence 8, Application US/09212971B  
 Patent No. 6107041  
 GENERAL INFORMATION:  
 APPLICANT: Korneluk, Robert G  
 APPLICANT: Mackenzie, Alexander E  
 APPLICANT: Liston, Peter  
 APPLICANT: Baird, Stephen  
 APPLICANT: Tsang, Benjamin K  
 APPLICANT: Pratt, Christine  
 TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
 TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
 TITLE OF INVENTION: DISEASE  
 FILE REFERENCE: 07891/009002  
 CURRENT APPLICATION NUMBER: US/09/212,971B  
 EARLIER FILING DATE: 1998-12-16  
 EARLIER APPLICATION NUMBER: 60/017,354  
 EARLIER FILING DATE: 1996-04-26  
 EARLIER APPLICATION NUMBER: 60/030,590  
 EARLIER FILING DATE: 1996-11-14  
 EARLIER APPLICATION NUMBER: 08/800,929  
 EARLIER FILING DATE: 1997-02-13  
 NUMBER OF SEQ ID NOS: 17  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 8  
 LENGTH: 618  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-212-971-8

Query Match 39.0%; Score 48; DB 3; Length 618;  
 Best Local Similarity 50.0%; Pred. No. 10;  
 Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 4 ASSGQARFNPAPYLPSCLE 23  
 DB 236 AMSEHRRHFPNCPLFENSL 255

RESULT 14  
 US-08-800-929A-8  
 Sequence 8, Application US/08800929A  
 Patent No. 613437  
 GENERAL INFORMATION:  
 APPLICANT: Korneluk, Robert G  
 APPLICANT: Mackenzie, Alexander E  
 APPLICANT: Liston, Peter  
 APPLICANT: Baird, Stephen  
 APPLICANT: Tsang, Benjamin K  
 APPLICANT: Pratt, Christine  
 TITLE OF INVENTION: DETECTION AND MODULATION OF  
 TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERAT  
 TITLE OF INVENTION: DISEASE  
 NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Clark & Elbing LLP  
 STREET: 176 Federal Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/800,929A  
 FILING DATE: 13-FEB-1997

CLASSIFICATION: 424

Prior Application Data:  
 APPLICATION NUMBER: 60/030,590  
 FILING DATE: 14-NOV-1996  
 APPLICATION NUMBER: 60/017,354  
 FILING DATE: 26-APR-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Bleker-Brady, Kristina  
 REGISTRATION NUMBER:  
 REFERENCE/DOCKET NUMBER: 07891/009001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-428-0200  
 TELEFAX: 617-428-7045

INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 618 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-800-929A-8

Query Match 39.0%; Score 48; DB 3; Length 618;  
 Best Local Similarity 50.0%; Pred. No. 10;  
 Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 4 ASSGQARFNPAPYLPSCLE 23  
 DB 236 AMSEHRRHFPNCPLFENSL 255

RESULT 15  
 PCT-US96-12860-2  
 Sequence 2, Application PC/TUS9612860  
 GENERAL INFORMATION:  
 APPLICANT: TUDARIK, INC.  
 TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: FLEHR, HOBACH, TEST, ALBRITTON & HERBERT  
 STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/12860  
FILING DATE: 06 AUG 1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brezner, David J.  
REGISTRATION NUMBER: 24,774  
REFERENCE/DOCKET NUMBER: A-62464/DJB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)781-1989  
TELEFAX: (415)398-3249  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 618 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-12860-2

Query Match 39.0%; Score 48; DB 4; Length 618;  
Best Local Similarity 50.0%; Pred. No. 10;  
Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;  
QY 4 ASSGQARMPFNAPYLPSCLE 23  
DB 236 AMSEHRRHFNCPFLNSLE 255

Search completed: April 11, 2001, 14:02:12  
Job time: 517 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: April 11, 2001, 13:53:18 ; Search time 15.5 Seconds  
(without alignments)  
50.739 Million cell updates/sec

Title: US-09-164-223-2  
Perfect score: 123  
Sequence: 1 PSQASSGQARMPNAPLPSCLE 23

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

A\_Geneseq\_36.\*  
1: /SIDSL/gcgdata/geneseq/geneseq/AA1980.DAT:\*  
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3: /SIDSL/gcgdata/geneseq/geneseq/AA1982.DAT:\*  
4: /SIDSL/gcgdata/geneseq/geneseq/AA1983.DAT:\*  
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6: /SIDSL/gcgdata/geneseq/geneseq/AA1985.DAT:\*  
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8: /SIDSL/gcgdata/geneseq/geneseq/AA1987.DAT:\*  
9: /SIDSL/gcgdata/geneseq/geneseq/AA1988.DAT:\*  
10: /SIDSL/gcgdata/geneseq/geneseq/AA1989.DAT:\*  
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20: /SIDSL/gcgdata/geneseq/geneseq/AA1999.DAT:\*  
21: /SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	123	100.0	23	21	Y98502 Human WTI peptide
2	123	100.0	23	21	Y98503 Wtlms' tumour poly
3	123	100.0	154	19	W47175 Wtlms' tumour anti
4	123	100.0	210	16	R85066 Wtlms' tumour prot
5	123	100.0	210	18	W22883 Wtlms' tumour gene
6	123	100.0	345	12	R12240 Wtlms' tumour poly
7	123	100.0	429	19	W47173 Wtlms' tumour WTI
8	123	100.0	429	16	R85065 Wtlms' tumour poly
9	123	100.0	449	21	W47176 Human WTI protein
10	123	100.0	449	21	Y98804 Mouse WTI protein
11	123	100.0	449	21	Y98805 Mouse Wtlms' tumou
12	123	100.0	449	21	Y80196

13	123	100.0	449	21	Y80197 Human Wtlms' tumou
14	55	44.7	9	21	Y98810 WTI related peptid
15	53	43.1	9	21	Y98809 WTI related peptid
16	52	42.3	9	21	Y98564 WTI derived immuno
17	52	42.3	9	21	Y98629 WTI derived immuno
18	52	42.3	9	21	Y98752 WTI derived immuno
19	52	42.3	9	21	Y98767 WTI derived immuno
20	51	41.5	9	21	Y94202 Human cytotoxic T
21	51	41.5	9	21	Y98570 WTI derived immuno
22	51	41.5	9	21	Y98778 WTI related peptid
23	51	41.5	9	21	Y98811 Human Wtlms' tumou
24	51	41.5	9	21	Y80200 WTI derived immuno
25	51	41.5	9	21	Y98808 WTI derived immuno
26	49	39.8	9	21	Y98583 WTI related peptid
27	48	39.0	9	21	Y98583 WTI derived immuno
28	48	39.0	9	21	Y98697 Human IGFBP-5, Sy
29	48	39.0	9	21	Y98754 Human IGFBP-5, Sy
30	48	39.0	272	13	R26995 Human inhibitor of
31	48	39.0	438	17	W04563 Human c-14p1, Hom
32	48	39.0	618	18	W19746 Human HTP-2 prote
33	48	39.0	618	18	W19583 Human cellular inh
34	48	39.0	618	18	W13545 Insulin-like growt
35	48	39.0	618	19	W69296 Human insulin-like
36	48	39.0	618	20	Y33998 Insulin like growt
37	47	38.2	113	20	Y25508 A human insulin-11
38	47	38.2	186	17	R95328
39	47	38.2	186	18	W3571
40	47	38.2	271	13	R26994
41	47	38.2	272	13	R25700
42	47	38.2	272	17	R55084
43	47	38.2	272	17	R95329
44	47	38.2	272	18	W35572
45	47	38.2	272	21	Y33969

#### ALIGNMENTS

RESULT 1	
Y98502	standard; Peptide: 23 AA.
XX	
AC	Y98502:
XX	
DT	31-JUL-2000 (first entry)
XX	
DE	Human WTI peptide SEQ ID NO:2.
XX	
KW	WT1; immunotherapy; immunogenic; malignant disease; cancer; leukaemia;
KW	metastatic disease; mouse; human; Wtlms' tumour; immune response;
KW	vaccine.
XX	
OS	Homo sapiens.
XX	
PN	W0200018795-A2.
XX	
PD	06-APR-2000.
XX	
PF	30-SEP-1999; 99WO-US22819.
XX	
PR	30-SEP-1998; 98US-0164223.
XX	
PR	25-MAR-1999; 99US-0276484.
XX	
PA	(CORI-) CORIXA CORP.
XX	
PA	(GALG/) GALGER A.
XX	
PI	Gaiger A, Cheever M;
XX	
DR	WPI; 2000-293107/25.
XX	
PT	Novel polypeptides comprising an immunogenic portion of a native WTI
PT	polypeptide, useful for inhibiting the development of malignant
PT	diseases associated with WTI expression e.g. leukemia or cancer
PT	



a role in transcription regulation. The polypeptide or immunogenic fragments of the polypeptide can be used to treat cancerous or precancerous conditions (especially Wilms' tumour), or to raise antibodies for diagnostic use. The product allow detection of risk of development of Wilms' tumour, e.g. in diseases such as WAGR and Denys-Drash syndrome, to be assessed prior to current methods of detection.

**SQ Sequence 154 AA;**

Query Match	100.0%	Score 123;	DB 19;	Length 154;
Best Local Similarity	100.0%;	Pred. No. 1.3e-12;		
Matches 23; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

```
OY      1 PSQASSGQARMEFNAPYLPSCLE 23
          |||||
Db      31 psgassgqarmfnpapylpscle 53
```

RESULT	4
R85066	
ID	R85066 standard; Protein; 210 AA.

AC	R85066;
XX	
DT	02-FEB-1996 (first entry)

DE Wilms' tumour antigen WT1-6F.  
XX  
KW Wilms' tumour; WT1-6F; monoclonal antibody; leukaemia

OS	Chimeric Homo sapiens;
OS	Chimeric synthetic.

Accession	Location/Qualifiers	key
FT	1..11	Peptide
FT	/label=	
FT	"histidine-fusion_peptide"	
FT	/note=	
FT	"hexa-histidine peptide used to facilitate fusion protein purification"	

FT	Protein	12..192
FT	/Label= WT1	
FT	peptide	193..219
FT		"vector-derived amino acids /note="

PN	W09529995-A1
XX	
PD	09-NOV-1995.

PF	25-APR-1995;	95WO-US05523.
XX		
PR	28-APR-1994;	94US-0234783

PA (WIST-) WISTAR INST ANATOMY & BIOLOGY  
XX  
PI Herlyn M, Morris J, Rauscher FJ, R

DR WPI; 1995-393072/50  
DR N-PSDB; T02462.

Monoclonal antibodies specific for Wt1s' tumour protein antigen Wt1  
- useful for detecting, monitoring and diagnosing malignancies  
characterised by expression of Wt1 protein, e.g. leukaemia  
Example 1: Page 37-38; 54pp; English.

CC Wllms; tumor antigen WT1-6F (R850566) is based on amino acid  
CC 1-181 of the native sequence, plus additional N- and C-terminal  
CC sequences, and is encoded by synthetic DNA (T07465) optimized for  
CC expression in *E. coli*. WT1-6F is used to raise monoclonal  
CC antibodies specific for WT1.

**SQ** Sequence 210 AA;

Query Match	100.0%;	Score 123;	DB 16;	Length 210;
Best Local Similarity	100.0%;	Pred. No. 1,9e-12;		
Matches	23;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0

```
QY      1 PSQASSGQARMFPNAPYLPSCLE 23  
        |||||  
Db     128 psqassgqarmfpnapylpscle 150
```

RESULT	5
W22883	
ID	W22883 standard; Protein; 210 AA.

AC	W22883;
XX	
DT	24-SEP-1997 (first entry)

DE Wilms' tumour protein antigen WT1-6F;  
XX Wilms' tumour; WT1; antigen; WT1-6F;  
KW Wilms' tumour; WT1; antigen; WT1-6F;

OS	Homo sapiens
OS	Synthetic.

Accession	Key	Location/Qualifiers
FT	Peptide	1..11
FT		/note= "hisridine fusion peptide to facilitate purification"
FT		

Protein	12..192
FT	/note= "amino acids 1-181 of WTI protein"
FT	193..210
FT	/note= "vector sequences added during cloning"

US5633142-A  
27-MAY-1997

28-APR-1994;	94US-0234783.
01-JUN-1995;	95US-0456307.
28-APR-1994;	94US-0234783.

AA (WIST-) WISTAR INST ANATOMY & BIOLOGY.  
PA  
XX  
BT  
herlyn M. Morris J. Rauscher FJ, R

WPI; 1997-297358/27  
N-PSDB; T75529.

aa Diagnosis of mesothelioma and monitoring of leukaemia therapy  
 pt using monoclonal antibodies against Wilms' tumour 1 antigen  
 pt  
 xx Example 1: Columns 17-20: 21pp: English.  
 ps

The present sequence is the Wilms' tumour protein antigen Wt1-6F, which comprises amino acids 1-181 of the Wilms' tumour 1 antigen (Wt1) protein. Wt1-6F can be used to raise monoclonal antibodies (Mab), e.g. H2, H7 and/or H17, which are secreted by the hybridoma cell lines AFCC 11598, 11599 and 11600. The Mab can be used to diagnose mesothelioma, prostate cancer, ovarian cancer or leukaemia by binding an antigen in a whole blood, serum, plasma, synovial fluid or tissue sample, or monitor therapy in leukaemia patients by binding an antigen in a whole blood, plasma, serum, urine or bone marrow sample, indicating the presence of active leukaemia cells.

Sequence	210 AA
50	

Query Match 100.0%; Score 123; DB 18; Length 210;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-12;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PSQASSGQARMFPNAPYLPSCLE 23  
 Db 128 psgassgqarmfpnapylpscle 150

## RESULT 6

R12240  
 ID R12240 standard; Protein; 345 AA.

AC R12240;

DT 15-AUG-1991 (first entry)

DE Wilm's tumour gene prod.

KW Wilm's tumour; monoclonal antibodies.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Domain 3..156 /label= proline/glutamine rich region

FT Domain 216..226 /label= zinc finger domain 1

FT Domain 227..246 /label= zinc finger domain 2

FT Domain 247..276 /label= zinc finger domain 3

FT Domain 277..304 /label= zinc finger domain 4

PN W09107509-A.

PD 30-MAY-1991.

PF 13-NOV-1990; 90MO-US06629.

PR 13-NOV-1989; 89US-0435780.

PA (MASI) MASSACHUSETTS INST TECH.

PI Call KM, Glaser TM, Ito CY, Buckler AJ, Pelletier J;

PI Haber DA, Rose EA, Housman DE;

DR WPI; 1991-178117/24.

DR N-PSDB; Q12020.

PT Nucleotide sequence of human chromosome 11 band 13 Wilm's tumour

PS locus - used to diagnose, quantify and treat Wilm's tumours

PS Disclosure: fig 3; 67pp; English.

CC This polypeptide is encoded by the Wilm's tumour (WT) gene which  
 CC maps to the 11p13 locus of human chromosome 11. It contains 4  
 CC zinc finger binding domains and a proline/glutamine rich region  
 CC and hence is thought to be involved in transcription regulation.  
 CC using this WT protein and the DNA, probes and antibodies can be  
 CC developed for diagnosing WT. Lesions similar to WT may also  
 CC be detected.

SO Sequence 345 AA;

Query Match 100.0%; Score 123; DB 12; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-12;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PSQASSGQARMFPNAPYLPSCLE 23  
 ID R12240 standard; Protein; 345 AA.

Db 33 psgassgqarmfpnapylpscle 55

## RESULT 7

W47173  
 ID W47173 standard; Protein; 345 AA.

AC W47173;

DT 01-JUN-1998 (first entry)

DE Wilm's tumour polypeptide (WT33).

KW Wilm's tumour; WT33; cancer treatment; antibody production; WAGR;

OS Denys-drash syndrome; WT1.

FH Key Location/Qualifiers

FT Region 3..156 /note= "proline and glutamine rich region"

PN US5726288-A.

PD 10-MAR-1998.

PF 02-AUG-1993; 93US-0102942.

PR 02-AUG-1993; 93US-0102942.

PR 13-NOV-1989; 89US-0435780.

PR 13-NOV-1990; 90US-0614161.

PA (MASI) MASSACHUSETTS INST TECHNOLOGY.

PI Breuning W, Buckler AJ, Call KM, Daryveau A, Glaser TM;

PI Haber DA, Housman DE, Ito CY, Pelletier J, Rose EA;

DR WPI; 1998-192828/17.

DR N-PSDB; V17060.

PT New Wilm's tumour polypeptide - useful for, e.g. cancer treatment

PS and antibody production

PS Claim 2; Fig 3; 42pp; English.

CC This is a new Wilm's tumour (WT33) polypeptide. The Wilm's tumour gene  
 CC (WT1) is associated with 11p13 locus on the human chromosome. This  
 CC polypeptide has a region rich in proline and glutamine (W47173)  
 CC indicating that it has a role in transcription regulation. The  
 CC polypeptide or immunogenic fragments of the polypeptide can be used to  
 CC treat cancerous or precancerous conditions (especially Wilm's tumour), or  
 CC to raise antibodies for diagnostic use. The product allow detection of  
 CC risk of development of Wilm's tumour, e.g. in diseases such as WAGR and  
 CC Denys-Drash syndrome, to be assessed prior to current methods of  
 CC detection.

SO Sequence 345 AA;

Query Match 100.0%; Score 123; DB 19; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-12;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PSQASSGQARMFPNAPYLPSCLE 23  
 Db 33 psgassgqarmfpnapylpscle 55

RESULT 8  
 ID R85065 standard; Protein; 429 AA.

R85065  
 AC R85065;



```

XX 02-FEB-1996 (first entry)
DT Wlms' tumour WT1 antigen.
DE Wlms' tumour WT1; monoclonal antibody; leukaemia.
XX Wlms' tumour; WT1; monoclonal antibody; leukaemia.
XX Homo sapiens.
OS WO9529995-A1.
XX 09-NOV-1995.
PD 25-APR-1995; 95WO-US05523.
XX 28-APR-1994; 94US-0234783.
XX (WIST-) WISTAR INST ANATOMY & BIOLOGY.
XX Herlyn M, Morris J, Rauscher FJ, Rodeck U.
XX WPI; 1995-393072/50.
DR N-PSDB; R85065.
XX Monoclonal antibodies specific for Wlms' tumour protein antigen WT1
PT - useful for detecting, monitoring and diagnosing malignancies
PT characterised by expression of WT1 protein, e.g. leukaemia
XX Claim 1; Page 42-43; 54pp; English.
XX The human Wlms' tumour antigen WT1 (sequence given in R85065) was used
CC as the basis for the design of a synthetic WT1 sequence (see R85066)
CC used to raise monoclonal antibodies specific for the antigen.
XX Sequence 429 AA:

Query Match          100.0%; Score 123; DB 16; Length 429;
Best Local Similarity 100.0%; Pred. No. 4,2e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMPNAPYLPSCLE 23
   |||||||||||||||||||
Db 117 psgassgqarmfnpaylpscle 139

RESULT 9
W47176
ID W47176 standard; Protein; 449 AA.
XX
XX W47176;
AC
XX 01-JUN-1998 (first entry)
DT
XX Wlms' tumour polypeptide (WT1).
DE
XX Wlms' tumour; WT1; cancer treatment; antibody production; WAGR;
KW Denys-drash syndrome; WT1.
XX Homo sapiens.
OS
XX US5726288-A.
XX 10-MAR-1998.
PD
XX 02-AUG-1993; 93US-0102942.
PF
XX 02-AUG-1993; 93US-0102942.
PR 02-AUG-1993; 93US-0102942.
PR 13-NOV-1989; 89US-0435780.
PR 13-NOV-1990; 90US-0614161.
XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
XX

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PI Bruening W, Buckler AJ, Call KM, Darveau A, Glaser TM;
PI Haber DA, Housman DE, Ito CY, Pelletier J, Rose EA;
XX WPI; 1998-192828/17.
XX New Wlms' tumour polypeptide - useful for, e.g. cancer treatment
XX and antibody production
XX
XX Disclosure; Columns 39-42; 42pp; English.
XX This is a Wlms' tumour (WT1) polypeptide. The Wlms' tumour gene
XX (WT1) is associated with 11p3 locus on the human chromosome. The
XX polypeptide or immunogenic fragments of the polypeptide can be used to
XX treat cancerous or precancerous conditions (especially Wlms' tumour), or
XX to raise antibodies for diagnostic use. The product allow detection of
XX risk of development of Wlms' tumour, e.g. in diseases such as WAGR and
XX Denys-Drash syndrome, to be assessed prior to current methods of
XX detection.
XX Sequence 449 AA:

Query Match          100.0%; Score 123; DB 19; Length 449;
Best Local Similarity 100.0%; Pred. No. 4,4e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMPNAPYLPSCLE 23
   |||||||||||||||||||
Db 117 psgassgqarmfnpaylpscle 139

RESULT 10
Y98804
ID Y98804 standard; Protein; 449 AA.
XX
XX Y98804;
AC
XX 31-JUL-2000 (first entry)
DT
XX Human WT1 protein sequence SEQ ID NO:319.
DE
XX WT1; immunotherapy; immunogenic; malignant disease; cancer; leukaemia;
XX metastatic disease; mouse; human; Wlms' tumour; Immune response;
XX vaccine.
XX Homo sapiens.
OS
XX WO200018795-A2.
XX 06-APR-2000.
PD
XX 30-SEP-1999; 99WO-US22819.
PF
XX 30-SEP-1998; 98US-0164223.
PR 25-MAR-1999; 99US-0276484.
XX
XX (CORI-) CORIXA CORP.
XX (GAIG/) GAIGER A.
XX Gaiger A, Cheever M;
XX WPI; 2000-293107/25.
XX
XX Novel polypeptides comprising an immunogenic portion of a native WT1
XX polypeptide, useful for inhibiting the development of malignant
XX diseases associated with WT1 expression e.g. leukemia or cancer
XX
XX Disclosure; Page 190-191; 193pp; English.
XX The present invention describes polypeptides (I) comprising an
XX immunogenic portion of a native Wlms' tumour gene product polypeptide,
XX WT1, (or variants of the immunogenic portion retaining the ability to
XX react with WT1-specific antisera and/or T-cell lines or clones) and
XX

```

CC comprising 16 consecutive amino acids (aa) or less of a native WT1  
 CC polypeptide. The polypeptides are useful therapeutically and to  
 CC manufacture medicaments for enhancing/inducing an immune response in  
 CC patients. The polypeptides, mimetics or polynucleotides can be included  
 CC with a carrier/excipient in pharmaceutical compositions or with a  
 CC non-specific immune response enhancer (e.g. an adjuvant or enhancer  
 CC preferentially enhancing a T cell response) in vaccines. Pharmaceutical  
 CC compositions and vaccines can be administered to human patients to  
 CC enhance or induce an immune response specific for WT1 or a cell  
 CC expressing WT1, useful to inhibit the development of malignant diseases  
 CC associated with WT1 expression, e.g. leukemia (especially acute/chronic  
 CC myeloid leukemia or acute lymphocytic leukemia) or cancer (especially  
 CC breast, lung, thyroid or gastrointestinal cancer, or a melanoma). Y98501  
 CC to Y98811 represent polypeptide sequences, and A13848 to A13862 represent  
 CC PCR primers, used in the exemplification of the present invention.

SO Sequence 449 AA;

Query Match 100.0%; Score 123; DB 21; Length 449;  
 Best Local Similarity 100.0%; Pred. No. 4,4e-12;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PSQASSGQARMPNAPYLPSCLE 23  
 |||  
 DB 117 psqassgqarmfnapylpsole 139

RESULT 11

Y98805 ID Y98805 standard; Protein; 449 AA.

AC Y98805;

DT 31-JUL-2000 (first entry)

DE Mouse WT1 protein sequence SEQ ID NO:320.

KW WT1; immunotherapy; immunogenic; malignant disease; cancer; leukaemia;  
 KW metastatic disease; mouse; human; Wilm's tumour; immune response;

OS Mus musculus.

PN W0200018795-A2.

PD 06-APR-2000.

PF 30-SEP-1999; 99WO-US22819.

PR 30-SEP-1998; 98US-0164223.

PR 25-MAR-1999; 99US-0276484.

PA (CORI-) CORIXA CORP.

PI (GALG/) GALGER A.

PI Galger A, Cheever M;

DR WPI; 2000-293107/25.

PT Novel polypeptides comprising an immunogenic portion of a native WT1  
 PT polypeptide, useful for inhibiting the development of malignant  
 PT diseases associated with WT1 expression e.g. leukemia or cancer -

PS Disclosure; Page 191-192; 193pp; English.

CC The present invention describes polypeptides (I) comprising an  
 CC immunogenic portion of a native Wilm's Tumour gene product polypeptide,  
 CC WT1, (or variants of the immunogenic portion retaining the ability to  
 CC react with WT1-specific antisera and/or T-cell lines or clones) and  
 CC comprising 16 consecutive amino acids (aa) or less of a native WT1  
 CC polypeptide. The polypeptides are useful therapeutically and to  
 CC manufacture medicaments for enhancing/inducing an immune response in

CC patients. The polypeptides, mimetics or polynucleotides can be included  
 CC with a carrier/excipient in pharmaceutical compositions or with a  
 CC non-specific immune response enhancer (e.g. an adjuvant or enhancer  
 CC preferentially enhancing a T cell response) in vaccines. Pharmaceutical  
 CC compositions and vaccines can be administered to human patients to  
 CC enhance or induce an immune response specific for WT1 or a cell  
 CC expressing WT1, useful to inhibit the development of malignant diseases  
 CC associated with WT1 expression, e.g. leukemia (especially acute/chronic  
 CC myeloid leukemia or acute lymphocytic leukemia) or cancer (especially  
 CC breast, lung, thyroid or gastrointestinal cancer, or a melanoma). Y98501  
 CC to Y98811 represent polypeptide sequences, and A13848 to A13862 represent  
 CC PCR primers, used in the exemplification of the present invention.

SO Sequence 449 AA;

Query Match 100.0%; Score 123; DB 21; Length 449;  
 Best Local Similarity 100.0%; Pred. No. 4,4e-12;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PSQASSGQARMPNAPYLPSCLE 23  
 |||  
 DB 117 psqassgqarmfnapylpsole 139

RESULT 12

Y80196 ID Y80196 standard; Protein; 449 AA.

AC Y80196;

DT 24-MAY-2000 (first entry)

DE Mouse Wilm's tumour suppressor gene WT1 product SEQ ID NO:1.

KW Wilm's tumour suppressor gene; WT1; cancer; antigen; vaccine; MHC;  
 KW major histocompatibility complex; leukaemia; tumour; antitumour.

OS Mus sp.

PN W0200006602-A1.

PD 10-FEB-2000.

PF 30-JUL-1999; 99WO-JP04130.

PR 31-JUL-1998; 98JP-0218093.

PA (SUGI/) SUGIYAMA H.

PI Sugiyama H, Oka Y;

DR WPI; 2000-195264/17.

PT Cancer antigens based on Wilm's tumor suppressor gene WT1 product or  
 PT peptide derivatives, for cancer vaccines in treating leukemia and solid  
 PT tumors e.g. stomach cancer, skin cancer, lung cancer and breast cancer

PS Claim 2; Page 38-40; 48pp; Japanese.

CC The present invention describes a cancer antigen containing the active  
 CC component of Wilm's tumour suppressor gene WT1 product, or partial  
 CC peptides, for cancer vaccines in treating leukaemia and solid tumours.  
 CC The cancer antigens are useful for cancer vaccines in treating  
 CC leukaemia, bone-marrow abnormal formation syndrome, malignant lymphoma,  
 CC multiple myeloma, stomach cancer, cancer of the large intestine, lung  
 CC cancer, breast cancer, blastoma, liver cancer, skin cancer, bladder  
 CC cancer, prostate cancer, uterus cancer, cervical cancer, or ovary  
 CC cancer. The present sequence represents the mouse Wilm's tumour  
 CC suppressor gene WT1 product.

SO Sequence 449 AA;

Query Match 100.0%; Score 123; DB 21; Length 449;  
 Best Local Similarity 100.0%; Pred. No. 4,4e-12;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PSQASSGQARMFPNAPYLPSCLE 23  
 |||  
 DB 117 psqassgqarmfpnapylpscle 139

# RESULT 13

ID Y80197 standard; protein; 449 AA.

XX Y80197;

DT 24-MAY-2000 (first entry)

XX Human Wilm's tumour suppressor gene WT1 product SEQ ID NO:2.

XX Wilm's tumour suppressor gene; WT1; cancer; antigen; vaccine; MHC;

XX major histocompatibility complex; leukaemia; tumour; antitumour.

XX Homo sapiens.

XX WO200006602-A1.

XX 10-FEB-2000.

XX 30-JUL-1999; 99WO-JP04130.

XX 31-JUL-1998; 98JP-0218093.

XX (SUGI/) SUGIYAMA H.

XX Sugiyama H, Oka Y;

XX WPI; 2000-195264/17.

XX Cancer antigens based on Wilm's tumor suppressor gene WT1 product or

XX peptide derivatives, for cancer vaccines in treating leukemia and solid

XX tumors e.g. stomach cancer, skin cancer, lung cancer and breast cancer

XX Claim 2; Page 40-42; 48pp; Japanese.

XX The present invention describes a cancer antigen containing the active

XX component of Wilm's tumour suppressor gene WT1 product, or partial

XX peptides, for cancer vaccines in treating leukaemia and solid tumours.

XX The cancer antigens are useful for cancer vaccines in treating

XX leukaemia, bone-marrow abnormal formation syndrome, malignant lymphoma,

XX multiple myeloma, stomach cancer, cancer of the large intestine, lung

XX cancer, breast cancer, blastoma, liver cancer, skin cancer, bladder

XX cancer, prostate cancer, uterus cancer, cervical cancer, or ovary

XX cancer. The present sequence represents the human Wilm's tumour

XX suppressor gene WT1 product.

XX Sequence 449 AA;

XX Query Match 100.0%; Score 123; DB 21; Length 449;

XX Best Local Similarity 100.0%; Pred. No. 4,4e-12;

XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 31-JUL-2000 (first entry)

XX WT1 related peptide SEQ ID NO:325.

XX WT1; immunotherapy; immunogenic; malignant disease; cancer; leukaemia;

XX metastatic disease; mouse; human; Wilm's tumour; immune response;

XX vaccine.

XX Homo sapiens.

XX Mus musculus.

XX WO200018795-A2.

XX 06-APR-2000.

XX 30-SEP-1999; 99WO-US22819.

XX 30-SEP-1998; 98US-0164223.

XX 25-MAR-1999; 99US-0276484.

XX (CORI-) CORIXA CORP.

XX (GAIG/) GAIGER A.

XX Galger A, Cheever M;

XX WPI; 2000-293107/25.

XX Novel polypeptides comprising an immunogenic portion of a native WT1

XX polypeptide, useful for inhibiting the development of malignant

XX diseases associated with WT1 expression e.g. leukemia or cancer

XX Disclosure; Page 193; 193pp; English.

XX The present invention describes polypeptides (I) comprising an

XX immunogenic portion of a native Wilm's Tumour gene product polypeptide,

XX WT1, (or variants of the immunogenic portion retaining the ability to

XX react with WT1-specific antisera and/or T-cell lines or clones) and

XX comprising 16 consecutive amino acids (aa) or less of a native WT1

XX polypeptide. The polypeptides are useful therapeutically and to

XX manufacture medicaments for enhancing/inducing an immune response in

XX patients. The polypeptides, mimetics or polynucleotides can be included

XX with a carrier/exipient in pharmaceutical compositions or with a

XX non-specific immune response enhancer (e.g. an adjuvant or enhancer

XX preferentially enhancing a T cell response) in vaccines. Pharmaceutical

XX compositions and vaccines can be administered to human patients to

XX enhance or induce an immune response specific for WT1 or a cell

XX expressing WT1, useful to inhibit the development of malignant diseases

XX associated with WT1 expression, e.g. leukemia (especially acute/chronic

XX myeloid leukemia or acute lymphocytic leukemia) or cancer (especially

XX breast, lung, thyroid or gastrointestinal cancer, or a melanoma). Y98501

XX to Y98811 represent polypeptide sequences, and A13848 to A13862 represent

XX PCR primers, used in the exemplification of the present invention.

XX Sequence 9 AA;

XX Query Match 44.7%; Score 55; DB 21; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 2.1e-05;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX OY 13 PNAPYLPSC 21

XX |||

XX DB 1 pnapylpsc 9

XX RESULT 15

XX Y98809 standard; Peptide; 9 AA.

XX ID Y98809;

XX AC Y98809;

XX DT 31-JUL-2000 (first entry)

XX WT1 related peptide SEQ ID NO:324.  
DE  
XX

KW WT1: Immunotherapy; immunogenic; malignant disease; cancer; leukemia;  
metastatic disease; mouse; human; Wilm's tumour; Immune response;  
vaccine.  
XX

OS Homo sapiens.  
XX Mus musculus.  
XX

PN W0200018795-A2.  
XX

PD 06-APR-2000.  
XX

PF 30-SEP-1999; 99WO-US22819.  
XX

PR 30-SEP-1998; 98US-0164223.  
XX 25-MAR-1999; 99US-0276484.  
XX

PA (CORI-) CORIXA CORP.  
XX (GAIG/) GAIGER A.  
XX

PI Gaiger A, Cheever M;  
XX

DR WPI: 2000-293107/25.  
XX

PT Novel polypeptides comprising an immunogenic portion of a native WT1  
polypeptide, useful for inhibiting the development of malignant  
diseases associated with WT1 expression e.g. leukemia or cancer  
XX

PS Disclosure: Page 193; 193pp; English.  
XX

CC The present invention describes polypeptides (I) comprising an  
immunogenic portion of a native Wilm's Tumour gene product polypeptide,  
WT1. (Or variants of the immunogenic portion retaining the ability to  
react with WT1-specific antisera and/or T-cell lines or clones) and  
comprising 16 consecutive amino acids (aa) or less of a native WT1  
polypeptide. The polypeptides are useful therapeutically and to  
manufacture medicaments for enhancing/inducing an immune response in  
patients. The polypeptides, mimetics or polynucleotides can be included  
with a carrier/excipient in pharmaceutical compositions or with a  
non-specific immune response enhancer (e.g. an adjuvant or enhancer  
preferentially enhancing a T cell response) in vaccines. Pharmaceutical  
compositions and vaccines can be administered to human patients to  
enhance or induce an immune response specific for WT1 or a cell  
expressing WT1, useful to inhibit the development of malignant diseases  
associated with WT1 expression, e.g. leukemia (especially acute/chronic  
myeloid leukemia or acute lymphocytic leukemia) or cancer (especially  
breast, lung, thyroid or gastrointestinal cancer, or a melanoma). Y98501  
to Y98811 represent polypeptide sequences, and A13848 to A13862 represent  
PCR primers, used in the exemplification of the present invention.  
XX

XX  
SQ Sequence 9 AA;

Query Match

43.1%; Score 53; DB 21; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.1e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MFPNAPYLP 19

Db 1 mfpnapylp 9

Search completed: April 11, 2001, 14:01:57  
Job time: 519 sec